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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION**

Related Applications

5 This application claims priority to prior U.S. Provisional Patent Application
Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial
No. 60/143208, filed July 9, 1999, and U.S. Provisional Patent Application Serial No.
60/151572, filed August 31, 1999. This application also claims priority to prior German
Patent Application No. 19931412.8, filed July 8, 1999, German Patent Application No.
10 19931413.6, filed July 8, 1999, German Patent Application No. 19931419.5, filed July
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1999, German Patent Application No. 19942123.4, filed September 3, 1999, and
German Patent Application No. 19942125.0, filed September 3, 1999. The entire
30 contents of all of the aforementioned application are hereby expressly incorporated
herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals',
5 include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful
10 organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

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Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*
20 *glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in
25 industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the SMP nucleic acids of the
30 invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a

microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the
5 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain
10 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference
15 points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon
20 compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama
25 *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a
30 direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize
5 sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the
10 generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of
15 such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-
20 encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the
25 isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
30 SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ

ID NO:6, SEQ ID NO:8....).. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence
5 which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function
10 involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%,
15 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-
20 numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of
25 the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also
30 includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing) A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 782) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about
5 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively
10 linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in
15 *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a
20 substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical
25 is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or
30 *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, *e.g.*, pyruvate from modified *C. glutamicum*), or may have an indirect

impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

5 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids
10 (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals
15 do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical
20 industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine,
25 valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
30 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transfer of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own

production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

5

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are
10 either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications
15 of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor"
20 includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty
25 acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley
30 & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthanol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD
5 (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
10 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

15 Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a
20 pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA
25 synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical
30 indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of

enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen
5 foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from
10 many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic
15 compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose,
20 sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon sources, including alcohols (*e.g.*, ethanol or methanol), alkanes, sugar alcohols, fatty
25 acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J.
30 (1980) *Industrielle Mikrobiologie*, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. *Microbial Technology* 2nd ed., vol. 2, chapter 18, Academic Press: New York; and

Kockova-Kratachvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Parnas (EMP) pathway (also known as the glycolytic or fructose bisphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xylulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate.

Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

5 The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for
10 glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

 In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy
15 that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anaerobes, have evolved such that they
20 possess both of these pathways.

 The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by
25 the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

 The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate
30 cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO₂. The acetyl group of acetyl CoA then reacts with

the 4 carbon unit, oxaloacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO₂ molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing the cycle. The electrons released during the oxidation of intermediates in the TCA cycle
5 are transferred to NAD⁺ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept
10 electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH
15 dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine
20 dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport
25 chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (*e.g.*,
30 coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H^+ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (e.g., ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (e.g., ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (e.g., ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment,

the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid sequences encoding an SMP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term "degradation product" is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary for the biosynthesis of other compounds by the cell. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

10 In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of

reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C. glutamicum* SMP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention

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(e.g., the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (e.g., ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (e.g., SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the

genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and

appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*,
5 using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises
10 sequences encoding SMP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing.. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the
15 Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (*i.e.*, RXA01626, RXN00043, or RXS0735). Each of the nucleic acid sequences
20 comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, or
25 RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02735 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The
30 sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated

RXA00042 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00042, and the amino acid sequence designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043. The correspondence between the RXA, RXN and RXS nucleotide and
5 amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as
10 "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence
15 for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

20 In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is
25 sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
30 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%,

87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited
5 ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*,
10 hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer
15 or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises
20 substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of
25 one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.*
30 the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding

nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently
5 homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used
10 herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the
15 protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine
20 chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
25 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the SMP nucleic acid molecules of the invention
30 are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon

compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41),

a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to

5 calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the

10 lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%,

15 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SMP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (*e.g.*, the *C.*

20 *glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the

25 SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on

30 their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or
5 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about
10 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by
15 one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*,
20 encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to
25 changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (*e.g.*, an
30 even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential
5 for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the
10 invention and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-
15 70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of
20 the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one
25 sequence (*e.g.*, one of the amino acid sequences the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two
30 sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that

5 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid

10 substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine,

15 threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same

20 side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

25 the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which

30 are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or

complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-

galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-

methyribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are
5 capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be
10 designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No.
15 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*,
20 an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

25 B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid",
30 which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.

10 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells.

Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, T7-, T5-, T3-, *gal*-, *trc*-, *ara*-, SP6-, *amy*, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, *rp28*, ADH, promoters from plants such as CaMV/35S, SSU, OCS, *lib4*,

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usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors
5 of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes
10 can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic
15 Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis*
20 *thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

25 Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors
30 typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion

expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- 5 Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a
- 10 pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.
- 15 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 20 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
- 25 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
- 30 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another
5 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

10 In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and
15 methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier:
20 New York (ISBN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989)
25 *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
30 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+,

pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional

flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination
5 vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.
10 For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that
15 expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion,
20 truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

25 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has
30 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another

embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

5 Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes
10 preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein,
15 still more preferably less than about 10% of non-SMP protein, and most preferably less than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein
20 preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by
25 dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from
30 the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum*.

An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (*e.g.*, by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred

5 embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as

10 oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a

15 nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least

20 about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity

25 values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described

30 herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and

which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (e.g., ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

5 In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in
10 another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or
15 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of
20 identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an SMP protein include peptides comprising
25 amino acid sequences derived from the amino acid sequence of an SMP protein, e.g., an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at least one activity of an SMP protein.
30 Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other

biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

5 SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard
10 protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

15 The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a
20 protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of
25 the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian
30 host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
5 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide).
15 An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the
20 activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway
25 which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid
30 level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP

sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a
5 degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3;
10 Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding
15 sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by
20 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
25 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
30 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the

frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a
5 variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the
10 following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a
15 cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum*
20 or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.
25 Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli
30 secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and

spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

5 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of
10 *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as
15 markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
20 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the
25 invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which
30 the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the

evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein
5 engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in
10 greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism
15 expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production
20 of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar
25 compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the
30 genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit

unfavorable, yet desired metabolic reactions (e.g., the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO₂ production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum*.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (e.g., by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (e.g., nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

HMP:

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXS02735	VW0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

TCA:

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
9	10	RXN01312	VW0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13	14	RXN00231	VW0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

EMB-Pathway

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27	28	RXN02803	VW0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VW0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
51	52	RXA02122	GR00636	6511	5813	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
53	54	RXA02006	GR00032	6171	5134	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13)
59	60	RXA01702	GR00479	1397	366	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
61	62	RXA02258	GR00654	28451	27227	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
63	64	RXN01225	VV0064	6382	4943	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
67	68	RXA02256	GR00654	23934	24935	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
69	70	RXA02257	GR00654	25155	26369	ENOLASE (EC 4.2.1.11)
71	72	RXA00235	GR00036	2365	1091	PYRUVATE KINASE (EC 2.7.1.40)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2.7.1.40)
75	76	RXN02675	VV0098	72801	70945	PYRUVATE KINASE (EC 2.7.1.40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1.40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2.7.1.40)
81	82	RXA00682	GR00179	5299	3401	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
85	86	RXA00635	VV0135	22708	20972	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
91	92	RXN03044	VV0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
97	98	RXN03086	VV0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
101	102	RXN03043	VV0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
103	104	F RXA02897	GR10039	1291	5	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
105	106	RXN03083	VV0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
107	108	F RXA02853	GR10001	89	1495	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	RXN02326	VV0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
113	114	F RXA02326	GR00688	5338	4523	PYRUVATE CARBOXYLASE
115	116	RXN02327	VV0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
117	118	F RXA02327	GR00688	6305	5346	PYRUVATE CARBOXYLASE
119	120	RXN02328	VV0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
121	122	F RXA02328	GR00688	7783	6401	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
123	124	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
131	132	RXN00296	W0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
135	136	RXA01901	GR00544	4158	5417	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
137	138	RXN01952	W0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
141	142	F RXA01955	GR00562	4611	6209	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
145	146	RXN01130	W0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
149	150	RXN03112	W0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
153	154	RXN00871	W0127	3127	2240	IOLB PROTEIN
155	156	F RXA00871	GR00239	2344	3207	IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE
157	158	RXN02829	W0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	W0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	W0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
171	172	RXN02688	W0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
173	174	RXN03087	W0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
175	176	RXN03186	W0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
177	178	RXN03187	W0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
179	180	RXN02591	W0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	W0009	3477	2296	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	W0009	3703	3533	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187	188	RXN01025	W0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

Glycerol metabolism

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
197	198	RXN01891	VW0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VW0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2.7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC 1.1.1.1)
219	220	RXN03061	VW0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221	222	RXN03150	VW0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223	224	RXN01340	VW0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225	226	RXN01498	VW0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227	228	RXN02674	VW0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229	230	RXN00888	VW0127	2230	320	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
231	232	RXN01143	VW0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233	234	RXN01146	VW0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
235	236	RXN01144	VW0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)

Butanediol, diacetyl and acetoin formation

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
239	240	RXA02453	GR00710	6103	5351	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
241	242	RXS01758	VW0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Table 1 (continued)

HMP-Cycle

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)

Nucleotide sugar conversion

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
261	262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)
267	268	RXA01259	GR00367	987	130	UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9)
269	270	RXA02028	GR00616	573	998	UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (EC 2.7.7.27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
285	286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)

Inositol and ribitol metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXN00013	VW0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VW0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VW0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VW0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VW0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VW0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXN02654	VW0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VW0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VW0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VW0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VW0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1.-)
341	342	F RXA00309	GR00053	316	5	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
343	344	RXN00310	VW0006	6616	7050	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
353	354	RXN01369	VW0124	595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363	364	RXN01884	VW0184	1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
365	366	F RXA01884	GR00539	3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
367	368	RXA01111	GR00306	16981	17427	GLYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-)
369	370	RXN01550	VW0143	14749	16260	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
371	372	F RXA01550	GR00431	3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
373	374	RXN02100	VW0318	2	2326	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
375	376	F RXA02100	GR00631	3	920	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
377	378	F RXA02113	GR00633	2	1207	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
379	380	RXA02147	GR00639	15516	16532	ALPHA-AMYLASE (EC 3.2.1.1)
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)
383	384	RXA01888	GR00539	4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385	386	RXN01927	VW0127	50623	49244	XYLULOSE KINASE (EC 2.7.1.17)
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2.7.1.17)
389	390	RXA02729	GR00762	747	4	RIBOKINASE (EC 2.7.1.15)
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2.7.1.15)
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)
403	404	RXN01562	VW0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409	410	RXN00879	VW0099	8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase
413	414	RXN00043	VW0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
417	418	RXN01752	VW0127	35265	33805	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421	422	RXA01859	GR00529	1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
423	424	RXA00042	GR00007	2037	1279	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
425	426	RXA01482	GR00422	17271	15397	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (ISOMERIZING) (EC 2.6.1.16)
427	428	RXN03179	VW0336	2	667	URONATE ISOMERASE (EC 5.3.1.12)
429	430	F RXA02872	GR10013	675	4	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
431	432	RXN03180	VW0337	672	163	URONATE ISOMERASE (EC 5.3.1.12)
433	434	F RXA02873	GR10014	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435	436	RXA02292	GR00862	1611	2285	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)
437	438	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)
439	440	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
441	442	RXA02440	GR00709	5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
443	444	RXN01569	W0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
447	448	RXN02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	W0112	7004	6219	dtDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---)
457	458	RXA00327	GR00057	10263	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	W0135	28686	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
465	466	RXN03015	W0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
467	468	RXN03056	W0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
469	470	RXN03030	W0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
471	472	RXN00401	W0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	W0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	W0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	W0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	W0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	W0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
483	484	RXN01593	W0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	W0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	W0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS03215				GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
499	500	RXC00233	GR00006	1417	260	protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
527	528	RXC01659				protein involved in sugar metabolism
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism

TCA-cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4.1.3.7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549	550	RXN00519	VV0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553	554	RXN02209	VV0304	1	1671	ACONITATE HYDRATASE (EC 4.2.1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4.2.1.3)
557	558	RXN02213	VV0305	1378	2151	ACONITATE HYDRATASE (EC 4.2.1.3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1.3)
561	562	RXA02056	GR00625	3	2870	ACONITATE HYDRATASE (EC 4.2.1.3)
563	564	RXA01745	GR00495	2	1495	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
565	566	RXA00782	GR00206	3984	3103	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
569	570	RXN01695	VV0139	11307	12806	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573	574	F RXA01695	GR00474	4388	4179	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
575	576	RXA00290	GR00046	4693	5655	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
577	578	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
581	582	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
583	584	RXN03101	VV0066	2	583	MALIC ENZYME (EC 1.1.1.39)
585	586	RXN02046	VV0025	15056	14640	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
587	588	RXN00389	VV0025	11481	9922	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
						oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)

Table 1 (continued)

Glyoxylate bypass

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
589	590	RXN02399	VW0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VW0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1663	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
600	602	RXN03117	VW0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
601	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
603	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
605	608	RXA00512	GR00130	621	4	2-methylisocitrate synthase (EC 4.1.3.31)
607	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1.3.31)
609	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
611	614	RXN03144	VW0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
613	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
615	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	620	RXA02332	GR00671	1906	764	2-methylcitrate synthase (EC 4.1.3.31)
619	622	RXN02333	VW0141	901	1815	methylisocitrate lyase (EC 4.1.3.30)
621	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
623	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

Methyl-Malonyl-CoA-Mutases

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
625	628	RXN00148	VW0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
627	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Table 1 (continued)

Others

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
631	634	RXN00317	VW0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639	640	RXN02461	VW0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
641	642	RXN01744	VW0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)
653	654	RXN02480	VW0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
665	666	RXA02144	GR00639	11025	12248	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
667	668	RXA02740	GR00763	7613	8542	RIESKE IRON-SULFUR PROTEIN
669	670	RXA02743	GR00763	13534	12497	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
671	672	RXA01227	GR00355	1199	1519	CYTOCHROME AA3 CONTROLLING PROTEIN
673	674	RXA01865	GR00532	436	122	FERREDOXIN
675	676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677	678	RXA00679	GR00179	2302	1037	FERREDOXIN-NAD(+) REDUCTASE (EC 1.18.1.3)
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681	682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683	684	RXN00606	VW0192	11299	9026	NADH DEHYDROGENASE CHAIN L (EC 1.6.5.3)
685	686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE CHAIN L (EC 1.6.5.3)
687	688	RXN00595	VW0192	8642	7113	NADH DEHYDROGENASE CHAIN M (EC 1.6.5.3)
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE CHAIN M (EC 1.6.5.3)
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE CHAIN L (EC 1.6.5.3)
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE CHAIN L (EC 1.6.5.3)
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697	698	RXN00483	VW0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)

Redox Chain

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE
703	704	RXA00288	GR00046	2646	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA002741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN02560	VW0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN03014	VW0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VW0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VW0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VW0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VW0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QORC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03096	VW0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN02036	VW0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VW0317	3552	2794	Hypothetical Oxidoreductase
751	752	RXN02206	VW0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VW0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.1.-)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VW0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VW0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
767	768	RXN02821	VW0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	VW0090	4923	3274	ATP-BINDING PROTEIN

Cytochrome metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
779	780	RXN00684	VW0005	29864	28581	CYTOCHROME P450 116 (EC 1.14.-.-)
781	782	RXN00387	VW0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkf	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

	dcfAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651			
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

	Promoter and operator regions of tryptophan operon	
E01377		Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Suginoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranelate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIIR; clgIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cgIIIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock A ATP-binding protein	
U53587	aphA-3	3'-5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum fda</i> gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynebacteriophage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum lysA</i> gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mitrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,' <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	Lysine exporter protein; Lysine export regulator protein	Vrijic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z29563	thrC	Threonine synthase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

* A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence.	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rx00014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger napH, pur7, pur10, pur6, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rx00030	513	GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:AI497294	484	AI497294	fb63g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOOC P80961 ANTIFREEZE PROTEIN LS-12. ; mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rx00032	1632	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinol transporter (dalT), D-arabinol kinase (dalK), D-arabinol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rx00041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rx00042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996

Table 4 (continued)

rx000043 1287	GB_IN1:CEU33051	4899	U33051	Caenorhabditis elegans sur-2 mRNA, complete cds.	Caenorhabditis elegans	40,276	23-Jan-96
	GB_PAT:126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	97,591	07-OCT-1996
	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	97,591	08-OCT-1997 (Rel. 52, Created)
rx000098 1743	GB_PR3:AC005174	39769	AC005174	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence.	Homo sapiens	35,879	24-Jun-98
	GB_BA1:MSU88433	1928	U88433	Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	Mycobacterium smegmatis	62,658	19-Apr-97
	GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	37,638	27-Jul-98
rx00148 2334	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	36,784	17-Jun-98
	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	67,457	17-Jun-98
	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	40,883	03-DEC-1996
rx00149 1971	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis	67,457	10-DEC-1996
	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	Mycobacterium tuberculosis	35,883	03-DEC-1996
	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	Mycobacterium tuberculosis	51,001	10-DEC-1996
rx00195 684	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	51,001	17-Jun-98
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,735	19-Jun-98
	GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	57,014	15-Jun-96
rx00196 738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	41,892	19-Jun-98
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	41,841	19-Jun-98
	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	36,599	19-Jun-98
rx00202 1065	GB_RO:RATCBRQ	10752	M55532	Rat carbohydate binding receptor gene, complete cds.	Rattus norvegicus	36,212	27-Apr-93
	GB_EST11:AA253618	313	AA253618	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5' mRNA sequence.	Mus musculus	38,816	13-MAR-1997
	GB_EST26:A1390284	490	A1390284	mw96a03.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5' similar to TR:O09171 O09171 BETAIN-HOMOCYSTEINE METHYLTRANSFERASE.; mRNA sequence.	Mus musculus	42,239	2-Feb-99
rx00206 1161	GB_EST26:A1390280	467	A1390280	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5' mRNA sequence.	Mus musculus	37,307	2-Feb-99
	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	58,312	17-Sep-97
	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,632	23-Jun-99

Table 4 (continued)

GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
rx00224 1074	GB_BA1:BUJ32230	1769	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) and large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
GB_GSS11:AQ325043	734	AQ325043	mgxb0020J01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
GB_EST31:AI676413	551	AI676413	etmEST0167 EtH1 Eimeria tenella cDNA clone etmc074 5', mRNA sequence.	Eimeria tenella	35,542	19-MAY-1999
GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comp) gene, complete cds.	Acinetobacter sp. BD413	53,726	27-Sep-99
GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,688	29-Sep-97
GB_BA1:BACADHT	1688	D90421	B. stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus stearothermophilus	51,502	7-Feb-99
GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	42,875	17-Jun-98
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Pseudomonas sp. W7	49,898	03-MAR-1999
GB_GSS3:B16984	469	B16984	344A14.TVC CIT978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpL34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99
GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95

Table 4 (continued)

GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.	Homo sapiens	37,915	8-Nov-94
GB_EST32:A1734238	512	A1734238	zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN); mRNA sequence.	Homo sapiens	41,502	14-Jun-99
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
GB_EST15:AA531468	414	AA531468	nf63d12.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome.	variola minor virus	35,883	2-Sep-99
GB_VI:VARCG	186103	L22579	Varola major virus (strain Bangladesh-1975) complete genome.	Varola major virus	34,664	12-Jan-95
GB_VI:VVCGAA	185578	X69198	Varola virus DNA complete genome.	Varola virus	36,000	13-DEC-1996
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
GB_BA1:LCATPASEB	1514	X64542	L. casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
GB_BA1:LCATPASEB	1514	X64542	L. casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1998
GB_PR4:AC004916	129014	AC004916	Homo sapiens clone DJ0891L14, complete sequence.	Homo sapiens	38,549	17-Jul-99
GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	35,865	16-MAY-1998
GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
GB_PL2:AF112871	2394	AF112871	Astasia longa small subunit ribosomal RNA gene, complete sequence.	Astasia longa	36,465	28-Jun-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99

Table 4 (continued)

GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
GB_EST23:A1120939	561	A1120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone Mus musculus IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE); mRNA sequence.	Mus musculus	41,113	2-Sep-98
GB_EST23:A1120939	561	A1120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone Mus musculus IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381 Mouse calmodulin (MOUSE); mRNA sequence.	Mus musculus	41,113	2-Sep-98
GB_EST32:A1726450	565	A1726450	BNLGH15857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
GB_PR1:HSPAIP	1587	X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
GB_HTG1:AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,875	13-Sep-99
GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
GB_PR2:HSAP001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abliM, abliR genes and orfX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS *** 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98

Table 4 (continued)

	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
rx00517 1164	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_EST29:AI602158	481	AI602158	UI-R-ABO-vy-a-01-0-UI.s2 UI-R-ABO Rattus norvegicus cDNA clone UI-R-ABO- vy-a-01-0-UI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
rx00518 320	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
	GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphoenolpyruvate phosphonmutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
	GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome.	Escherichia coli	49,688	12-Nov-98
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
rx00635 1860	GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	34,347	21-Apr-97
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	53,912	14-Jul-95
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloclavata DNA for ORF 1.	Pseudomonas amyloclavata	54,422	14-Jul-95
rx00679 1389	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	38,244	13-Nov-99
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	36,165	30-Sep-98
rx00680 441	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
	GB_PL1:AB026648	43481	AB026648	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
rx00682 2022	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	37,143	28-Sep-99

Table 4 (continued)

rx00683	1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
		GB_IN1:DMBR7A4	212734	AL109630	Drosophila melanogaster clone BACR7A4.	Drosophila melanogaster	36,454	30-Jul-99
		GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rx00686	927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_EST12:AA284399	431	AA284399	zs57b04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rx00700	927	GB_EST34:AI785570	454	AI785570	uj44d03.x1 Sugano mouse liver mliia Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	41,943	2-Jul-99
		GB_EST25:AI256147	684	AI256147	ui95e12.x1 Sugano mouse liver mliia Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	Mus musculus	40,791	12-Nov-98
rx00703	2409	GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	37,721	23-Apr-91
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,369	19-Jun-98
		GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
rx00705	1038	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
		GB_EST11:AA224340	443	AA224340	zr14e07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
		GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rx00782	1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
		GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
		GB_BA2:AF128399	2842	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds.	Pseudomonas aeruginosa	53,698	25-MAR-1999
rx00783	1395	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS *** 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS *** 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
rx00794	1128	GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	35,864	8-Aug-98
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99

Table 4 (continued)

GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene, pseudogene similar to ribosomal protein L39, RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
rx00799 1767						
GB_PL2:AF016327	616	AF016327	Hordeum vulgare Barper1 (perm1) mRNA, partial cds.	Hordeum vulgare	41,311	01-OCT-1997
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,845	30-Nov-99
GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,845	30-Nov-99
rx00800 1227						
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	63,101	17-Jun-98
GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	41,312	13-Nov-98
GB_PL1:SCSFAARP	7008	X68020	S.cerevisiae SFA and ARP genes.	Saccharomyces cerevisiae	36,288	29-Nov-94
rx00825 1056						
GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	39,980	17-Jun-98
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,435	27-Aug-99
GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
rx00871						
rx00872 1077						
GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans cosmid F23H12, complete sequence.	Caenorhabditis elegans	34,502	08-OCT-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***; 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***; 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
rx00879 2241						
GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome; segment 81/162.	Mycobacterium tuberculosis	36,981	19-Jun-98
GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis ACT1 gene, exons 1-2.	Candida dubliniensis	38,716	1-Sep-99
GB_PL1:CAACT1A	3206	X16377	Candida albicans act1 gene for actin.	Candida albicans	36,610	10-Apr-93
rx00909 955						
GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	51,586	12-MAY-1998
GB_BA1:RIMPHA	7888	X93358	Rhizobium meliloti pha[A,B,C,D,E,F,G] genes.	Sinorhizobium meliloti	48,367	12-MAR-1999
GB_EST16:C23528	317	C23528	C23528 Japanese flounder spleen Paralichthys olivaceus cDNA clone HB5(2), mRNA sequence.	Paralichthys olivaceus	41,640	28-Sep-99
rx00913 2118						
GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***; 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99

GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44 O. 1 map 18, ***

GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_Q_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
GB_EST18:AA709478	406	AA709478	w34a05.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1224272 5', mRNA sequence.	Mus musculus	42,065	24-DEC-1997
GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
GB_BA1:MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	36,218	17-Jun-98
GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	98,349	24-Jun-98
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,120	17-Jun-98
GB_BA1:SCTA1	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
GB_BA1:MSGB1723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
GB_BA2:AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
GB_BA1:BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
GB_VI:HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	human herpesvirus 2	38,081	04-DEC-1998
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 653C5 on chromosome 1p21.3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence.	Homo sapiens	36,462	23-Nov-99
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	36,528	14-Jul-98

Table 4 (continued)

GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17. TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18. TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
GB_BA1:CORPYK1	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98
GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998
GB_GSS1:FR0005503	619	Z89313	F. rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	Fugu rubripes	37,785	01-MAR-1997
GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B3218, complete sequence.	Homo sapiens	35,835	10-Jul-98
GB_PR3:HS1178121	62268	AL109852	Human DNA sequence from clone RP5-1178121 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
GB_BA1:CGASO19	1452	X76875	C. glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	27-OCT-1994
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
GB_BA1:CGASO19	1452	X76875	C. glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
GB_VI:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).	Hepatitis C virus	36,769	5-Apr-92

rxa01200

Table 4 (continued)

rx01201 1764	GB_BA1:SLATPSYNA	8560	Z22606	S. lividans i protein and ATP synthase genes.	Streptomyces lividans	66,269	01-MAY-1995
	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995
rx01202 1098	GB_BA1:SLATPSYNA	8560	Z22606	S. lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995
	GB_BA1:SLATPSYNA	8560	Z22606	S. lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995
	GB_BA1:MCSQSSHC	5538	Y09978	M. capsulatus orf, orf, orf, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998
rx01204 933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain: Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS *** , 39 unordered pieces.	Homo sapiens	35,459	04-DEC-1999
	GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS *** , 39 unordered pieces.	Homo sapiens	36,117	04-DEC-1999
rx01216 1124	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98
	GB_BA2:AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998
	GB_BA1:CCRFLBDBA	4424	M69228	C. crescentus flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93
rx01225 1563	GB_BA2:AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** , 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
	GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** , 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
rx01227 444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	64,908	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	61,712	10-DEC-1996
rx01242 900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	35,373	09-OCT-1998
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99
	GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99

Table 4 (continued)

rx01243	1083	GB_GSS10: AQ255057	583	AQ255057	mgxb0008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008N01r, genomic survey sequence.	Magnaporthe grisea	38,722	23-OCT-1998
rx01259	981	GB_IN1: CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,448	23-Nov-98
		GB_IN1: CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,694	23-Nov-98
		GB_BA1: CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
		GB_HTG4: AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, *** SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
rx01262	1284	GB_HTG4: AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, ***SEQUENCING IN PROGRESS ***; 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
		GB_BA2: AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999
		GB_BA2: ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds.	Escherichia coli	59,735	5-Nov-97
		GB_BA1: D90841	20226	D90841	E. coli genomic DNA, Kohara clone #351(45.1-45.5 min.).	Escherichia coli	37,904	21-MAR-1997
rx01311	870	GB_PR3: AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
rx01312	2142	GB_HTG3: AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
		GB_HTG3: AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
		GB_BA2: AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
		GB_BA1: MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
		GB_BA1: U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
		GB_HTG4: AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
rx01325	795	GB_HTG4: AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
		GB_HTG4: AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
		GB_HTG6: AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPCI-98 03.D.6 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
		GB_HTG6: AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPCI-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999

Table 4 (continued)

GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPC111-375120, *** SEQUENCING IN PROGRESS ***; 25 Homo sapiens unordered pieces.	34,821	16-Sep-99
GB_BA2:AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.	58,487	19-OCT-1999
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	37,963	25-Feb-99
GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	37,963	25-Feb-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	38,011	17-Jun-98
GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucosyltransferase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	47,726	26-Apr-93
GB_GSS10:AQ194038	697	AQ194038	RPC111-47D24, T.J RPC11-11 Homo sapiens genomic clone RPC11-11-47D24, genomic survey sequence.	36,599	20-Apr-99
GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	36,940	17-Jun-98
GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	35,284	14-MAY-1997
GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	38,324	14-MAY-1997
GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,778	10-Feb-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	32,658	16-Nov-99
GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	38,395	16-Nov-99
GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4: putative transcriptional regulator, putative ferredoxin, putative cytochrome oxidoreductase, and putative oxidoreductase genes, complete unknown genes.	55,221	8-Jul-98
GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	100,000	24-Feb-97
GB_PR4:AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPC111-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	36,756	30-Jan-99
GB_BA1:CGPTAACKA	3657	X89084	C. glutamicum pta gene and ackA gene.	100,000	23-MAR-1999
GB_BA1:D90861	14839	D90861	E. coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	53,041	29-MAY-1997
GB_PAT:E02087	1200	E02087	DNA encoding acetate kinase protein from Escherichia coli.	54,461	29-Sep-97
GB_GSS1:HPU60627	280	U60627	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence.	39,286	9-Apr-97
GB_EST31:AI701691	349	AI701691	we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	39,412	3-Jun-99

Table 4 (continued)

GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to gbL19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);,, mRNA sequence.	Homo sapiens	39,574	14-Aug-97
GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	54,141	16-Aug-99
GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	38,126	05-MAY-1999
GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,852	9-Apr-97
GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	62,149	20-Aug-98
GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,303	01-MAR-1994
GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,179	18-Jun-98
rxa01534						
GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	66,208	27-Aug-99
GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	38,553	24-Jun-99
GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumC and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	52,690	23-OCT-1996
GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	56,487	7-Feb-99
GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	55,100	1-Jul-99
GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (GlyP) mRNA, complete cds.	Drosophila melanogaster	56,708	27-Apr-99
rxa01562						
GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence.	Streptomyces venezuelae	38,587	28-OCT-1998
GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (pick) gene, complete cds.	Streptomyces venezuelae	38,621	15-OCT-1998
GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98
GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (mlbB), glucose-1-phosphate thymidyl transferase (rmIA), dTDP-4-keto-L-rhamnose reductase (rmID), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmIC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	59,714	4-Nov-98

Table 4 (continued)

rxa01571 723	GB_BA2:NGOCPSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene.	Neisseria meningitidis	58,384	30-Jul-96
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
rxa01572 615	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
rxa01606 2799	GB_VI:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
	GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
	GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98
rxa01626 468	GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
	GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99
rxa01632 1128	GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
rxa01633 1206	GB_GSS8:B99182	415	B99182	CIT-HSP-2280113.TR CIT-HSP Homo sapiens genomic clone 2280113, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	36,591	26-Nov-97
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	34,941	26-Nov-97
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR4810 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99

Table 4 (continued)

rx01695 1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
	GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
rx01702 1155	GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95
	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
rx01743 901	GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
	GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
	GB_EST24:A1167112	579	A1167112	xylem.est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
	GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
rx01744 1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
	GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence.	Mycobacterium tuberculosis	63,438	31-Jul-97
rx01745 836	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,081	17-Jun-98
	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
rx01758 1140	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
	GB_PL3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
	GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
	GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
rx01814 1785	GB_BA1:ABCCCLB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds.	Acetobacter xylinus	62,173	21-Sep-94
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
rx01851 1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
	GB_IN2:AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
	GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99

Table 4 (continued)

rx01859 1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
	GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPCI93-25N14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rx01865 438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
	GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
rx01882 1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,899	27-Apr-93
	GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98
	GB_GSS3:B42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rx01884 1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
rx01886 897	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234.	Synechocystis sp.	47,792	7-Feb-99
	GB_GSS9:AQ116291	572	AQ116291	RPCL11-49P6.TK.1 RPCL11 Homo sapiens genomic clone RPCL11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
	GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
	GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rx01887 1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
	GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwofii wcz, wzb, wza, weeA, weeB, weeC, wzc, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU,ugd, pgj, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwofii	39,640	01-OCT-1999
rx01888 658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCL98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99

Table 4 (continued)

GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain Y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	32,969	2-Aug-99
GB_EST36:AI881527	598	AI881527	***, 113 unordered pieces.			
GB_EST36:AI881527	598	AI881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, Zea mays mRNA sequence.		43,617	21-Jul-99
GB_VI:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	Human immunodeficiency virus type 1	40,040	05-MAR-1999
GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Aspergillus fumigatus	37,844	1-Apr-97
GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Homo sapiens	37,136	2-Jun-98
GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Corynebacterium glutamicum	100,000	24-Apr-99
GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
GB_BA1:MSG838COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
GB_BA1:SCE63	37200	AL035640	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7qtel0 BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.R.L. B3728 xylA gene for D-xylose(D-glucose) isomerase. Arthrobacter sp.		56,283	04-MAY-1992
GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***; 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
GB_EST28:AI519629	612	AI519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98
GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgIA gene for phosphoglucosyltransferase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21); from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
GB_BA1:XSXCRBA	3161	X67744	S.xylosus scrB and scrR genes.	Staphylococcus xylosus	67,778	28-Nov-96
GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21); from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
GB_BA1:MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98

Table 4 (continued)

	GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
	GB_GSS13:AQ501177	767	AQ501177	V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', genomic survey sequence.	Saccharomyces cerevisiae	32,039	29-Apr-99
rxa02054	1140	GB_BA1:MLCB1222	34714	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
		GB_BA1:MTY13E12	43401	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
rxa02056	2891	GB_BA1:MTU43540	3453	Mycobacterium tuberculosis rfaA, rhamnose biosynthesis protein (rfaA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
		GB_PAT:E14601	4394	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
		GB_BA1:D84102	4394	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
		GB_BA1:MTV006	22440	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
rxa02061	1617	GB_HTG7:AC005883	211682	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
		GB_PL2:ATAC003033	84254	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
		GB_PL2:ATAC002334	75050	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
rxa02063	1350	GB_BA1:SCGLGC	1518	S.coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
		GB_GSS4:AQ687350	786	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone	Oryza sativa	40,696	1-Jul-99
		GB_EST38:AW028530	444	nbxb0074H11r, genomic survey sequence.	Homo sapiens	36,795	27-OCT-1999
rxa02100	2348	GB_BA1:MSGY151	37036	wv27f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similar to WP:T03G11.6 CE04874.; mRNA sequence.	Homo sapiens	40,156	10-DEC-1996
		GB_BA1:MTCY130	32514	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	55,218	17-Jun-98
		GB_BA1:SCO001205	9589	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,475	29-MAR-1999
		GB_BA1:D90858	13548	Streptomyces coelicolor A3(2) glycogen metabolism clusterl.	Streptomyces coelicolor	38,586	29-MAY-1997
rxa02140	1200	GB_EST37:A1948595	469	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	37,259	6-Sep-99
		GB_HTG3:AC010387	220665	wq07d12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3', mRNA sequence.	Homo sapiens	38,868	15-Sep-99
		GB_BA1:MSGB1551CS	36548	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***; 77 unordered pieces.	Homo sapiens	51,399	15-Jun-96
		GB_BA1:MSGB1554CS	36548	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
rxa02142	774	GB_RO:AF093099	2482	Mycobacterium leprae cosmid B1554 DNA sequence.	Mus musculus	36,683	01-OCT-1999
		GB_BA1:MTCY190	34150	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mycobacterium tuberculosis	57,292	17-Jun-98

Table 4 (continued)

GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999
GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone C17978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone C17978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
GB_EST28:AI492095	485	AI492095	tg07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
GB_EST10:AA157467	376	AA157467	zo50a01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_EST10:AA157467	376	AA157467	zo50a01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 ; mRNA sequence.	Mus musculus	39,715	2-Jul-99
GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acr), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998

Table 4 (continued)

rx02213 874	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasins 1 (inv1), invasins 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferredoxinase (mav272) genes, complete cds.	Mycobacterium avium	36,885	26-MAR-1998
rx02245 780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-bisphosphate aldolase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycerate phosphatase (cbbZ), and cbbY genes, complete cds.	Rhodobacter capsulatus	48,701	28-OCT-1997
rx02256 1125	GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
	GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone hRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
rx02257 1338	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
	GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
rx02258 900	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
rx02259 2895	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
	GB_BA1:CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93

Table 4 (continued)

rx02288 969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
	GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
rx02292 798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999
	GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Homo sapiens	39,185	16-Jul-99
	GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97
rx02322 511	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	57,677	17-Jun-98
	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98
rx02326 939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	37,363	17-Jun-98
rx02327 1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997
	GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	41,317	17-Jun-98
rx02328 1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
	GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
rx02332 1266	GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
	GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cys) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
rx02333 1038	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
	GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99

Table 4 (continued)

rx02399 1467	GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
	GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
rx02404 2340	GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
	GB_BA1:CGACEB	3024	X78491	C.glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
	GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
	GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
rx02414 870	GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
rx02435 681	GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
	GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,061	27-Apr-93
	GB_OM:RABPLASISM	4458	M64656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
rx02440 963	GB_EST14:AA417723	374	AA417723	zV01b12.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element; contains element L1 repetitive element 1, mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
	GB_EST11:AA215428	303	AA215428	z195a07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element; mRNA sequence.	Homo sapiens	39,934	13-Aug-97
	GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
rx02453 876	GB_EST14:AA426336	375	AA426336	zV53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3', mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
	GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
	GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
rx02474 897	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2,3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
	GB_OM:BTU71200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
	GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
rx02480 1779	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99

Table 4 (continued)

rx02485	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
	GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 3/7.	Aeropyrum pernix	48,014	22-Jun-99
rx02492 840	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	Streptomyces coelicolor	65,672	26-Apr-93
	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
rx02528 1098	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
rx02539 1641	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_BA2:RSU17129	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
rx02551 483	GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	65,174	17-Jun-98
	GB_BA2:AF068264	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
rx02556 1281	GB_BA1:BACHYPTP	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BACHUTWAP#28954	D31856	D31856	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BSGBGLUC	4290	Z34526	B. subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	Bacillus subtilis	53,602	3-Jul-95
	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
rx02560 990	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_PL2:AC005292	99053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	36,420	2-Sep-99
	GB_EST32:A731605	566	A1731605	BNLGH10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99

Table 4 (continued)

rx02572 668	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	61,677	17-Jun-98
	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	37,170	17-Jun-98
	GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLC116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	19,820	29-Sep-99
rx02596 1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
	GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
	GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rx02611 1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,532	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
	GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rx02612 2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,018	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	58,510	10-DEC-1996
	GB_BA1:STMGLGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rx02621 942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, antR gene and citE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
	GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence.	Caenorhabditis elegans	37,608	2-Sep-99
	GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rx02640 1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
	GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol diffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfX) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
rx02654 1008	GB_BA1:AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B7T7, mRNA sequence.	Arabidopsis thaliana	39,637	5-Jan-98
	GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence.	Arabidopsis thaliana	33,735	5-Aug-99
	GB_RO:MMU58105	88871	U58105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rx02666 891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998

Table 4 (continued)

GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	41,599	01-MAY-1998
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	40,413	1-Jul-98
GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds; biotin [acetyl-CoA carboxyl] ligase (bifA) gene, complete cds.	Paracoccus denitrificans	40,735	20-MAY-1993
GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	Mycobacterium tuberculosis	36,471	17-Jun-98
GB_BA1:MXADEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	Myxococcus xanthus	38,477	27-Jan-94
GB_BA1:BACLDH	1147	M19394	B. caldolyticus lactate dehydrogenase (LDH) gene, complete cds.	Bacillus caldolyticus	57,371	26-Apr-93
GB_BA1:BACLDHL	1361	M14788	B. stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	57,277	26-Apr-93
GB_PAT:A06664	1350	A06664	B. stearothermophilus lct gene.	Bacillus stearothermophilus	57,277	29-Jul-93
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	50,746	27-Jun-97
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	36,364	27-Jun-97
GB_EST19:AA758660	233	AA758660	ah67d06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence.	Homo sapiens	37,059	29-DEC-1998
GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence.	Danio rerio	42,149	27-Jun-97
GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,655	15-Nov-99
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580	24-Jun-98
GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363	19-Jun-98
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444	27-Jul-98
GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226	24-Jun-98
GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399	12-Jul-99
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	36,426	27-Jul-98
GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	99,640	20-Feb-99

Table 4 (continued)

	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	61,573	04-DEC-1998
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	61,573	01-MAR-1994
rx02740 1053	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
	GB_HTG3:AC007150	121474	AC007150	Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98 16.P.13 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 87 unordered pieces.	Drosophila melanogaster	38,728	20-Sep-99
rx02741 1089	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022114, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
rx02743 1161	GB_IN1:AB006546	931	AB006546	Ephydatia fluviatilis mRNA for G protein a subunit 4, partial cds.	Ephydatia fluviatilis	36,379	23-Jun-99
	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	48,401	04-DEC-1998
	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401	01-MAR-1994
rx02797 1026	GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	37,128	26-Jun-99
	GB_BA1:CGBETPGEN	2339	X93514	C.glutamicum betP gene.	Corynebacterium glutamicum	38,889	8-Sep-97
	GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.	Homo sapiens	34,321	08-OCT-1998
	GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	38,072	1-Feb-97
rx02803 680	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	34,462	01-MAR-1994
	GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MraA (mraA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.	Pseudomonas syringae pv. syringae	50,445	9-Apr-97
rx02821 363	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	59,314	20-Aug-98
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
	GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone Mus musculus 2610200J17, mRNA sequence.	Mus musculus	40,157	30-Jun-99

Table 4 (continued)

rx02829 373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
	GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rx03216 1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
	GB_EST15:AA477537	411	AA477537	zu35g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element; contains element HGR repetitive element.; mRNA sequence.	Homo sapiens	37,260	9-Nov-97
	GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5', mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rx03215 1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
	GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
	GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rx03224 1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
	GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
	GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

5

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

25

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

30

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. et al. (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin of replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. et al. (1985) *J. Bacteriol.* 162:591-597, Martin J.F. et al. (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. et al. (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. et al. (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. et al. (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schäfer, A et al.

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, e.g., DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (e.g., a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
25 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

- Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these 20 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- 25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotehnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. *Ulmann's Encyclopedia of Industrial Chemistry*, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid
5 molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped
10 BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-
15 17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described
20 in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap
25 weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present
30 in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

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were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For
20 example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

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may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (e.g., ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, e.g., Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (e.g., metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of
5 the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an SMP protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

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7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 5 18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.
- 10 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 15 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
- 20 by any of the F-designated genes set forth in Table 1.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 30 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

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sequences as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

- 5 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 10 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 15 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,
20 *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,
Corynebacterium acetophilum, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
Brevibacterium butanicum, *Brevibacterium divaricatum*, *Brevibacterium flavum*,
Brevibacterium healii, *Brevibacterium ketoglutamicum*, *Brevibacterium*
25 *ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
Brevibacterium paraffinolyticum, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
- 30 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

- 5 32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
10 tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
15
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 782 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1,
20 thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the
25 Sequence Listing, wherein the nucleic acid molecule is disrupted.
35. 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more
30 nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

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38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified
- 5 relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

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 Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val
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 His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
 105 110 115

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 Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
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 Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
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 Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
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Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
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 10 15 20

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 25 30 35

cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259
 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu
 40 45 50

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 Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln
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Ala Gln Gly Gly Val Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu
 35 40 45

Ala Gly Thr Ala Glu Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly
 50 55 60

Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His
 65 70 75 80

Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser
 85 90 95

Ala Glu Thr Phe Glu Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro
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Gly Leu Asn
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(757)

<223> RXA02245

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 Met Ala Gln Arg Thr
 1 5

cca cta atc gcc cca tcc att ctt gct gct gat ttc tcc cgc tta ggg 163
 Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly
 10 15 20

gag cag gtg ttg gct gtt cct gat gct gac tgg att cac gtc gac atc 211
 Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
 25 30 35

atg gac gga cac ttc gtt cca aac ttg agc ttt ggc gcg gat atc aca 259
 Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
 40 45 50

gct gcg gtc aac cgc gtt acg gac aaa gaa cta gac gtc cac ctg atg 307
 Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu Asp Val His Leu Met
 55 60 65

atc gaa aac cca gag aag tgg gtg gac aac tac atc gac gct ggc gcg 355
 Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala
 70 75 80 85

gac tgc att gtt ttc cac gtt gaa gcc acc gaa ggt cac gtt gag ttg 403
 Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
 90 95 100

gct aag tac atc cgt tcc aag ggt gtg cgt gca ggt ttc tcc ctg cgc 451
 Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala Gly Phe Ser Leu Arg
 105 110 115

cct gga act ccc atc gag gat tac ttg gat gac ctc gag cac ttc gat 499
 Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp
 120 125 130

gaa gtc atc gtc atg agc gtc gag cct gga ttc ggt ggc caa agc ttc 547
 Glu Val Ile Val Met Ser Val Glu Pro Gly Phe Gly Gly Gln Ser Phe
 135 140 145

atg cct gaa caa ctg gaa aag gtt cgt acc ctg cgc aag gtc atc gat 595
 Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu Arg Lys Val Ile Asp
 150 155 160 165

gag cgc ggt ctg aac acc gtc atc gag atc gac ggc ggc att agc gcc 643
 Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp Gly Gly Ile Ser Ala
 170 175 180

aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca 691
 Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
 185 190 195

ggt tcc gct gtg tac ggc gct gag gat ccc aac aag gcg atc cag gag 739
 Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn Lys Ala Ile Gln Glu
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 Leu Arg Ala Leu Ala Gln
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<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

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Phe Ser Arg Leu Gly Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp
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Ile His Val Asp Ile Met Asp Gly His Phe Val Pro Asn Leu Ser Phe
 35 40 45
 Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
 50 55 60
 Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
 65 70 75 80
 Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
 85 90 95
 Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
 100 105 110
 Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
 115 120 125
 Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
 130 135 140
 Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu
 145 150 155 160
 Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
 165 170 175
 Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val
 180 185 190
 Asp Ala Phe Val Ala Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn
 195 200 205
 Lys Ala Ile Gln Glu Leu Arg Ala Leu Ala Gln
 210 215

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 <213> Corynebacterium glutamicum

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 Met Arg Val Tyr Leu
 1 5

 gga gca gac cac gct ggt ttc gaa act aaa aat gca atc gca gaa cac 163
 Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His
 10 15 20

 ctt aag gcc cac ggc cac gaa gtg atc gac tgc gga gcc cac acc tat 211
 Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr

25 30 35
 gat gca gaa gat gac tac cca gcc ttc tgc atc gaa gca gct agc cgc 259
 Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile Glu Ala Ala Ser Arg
 40 45 50
 aca gta aac gac cca ggc tca ctc ggc atc gtc ctg ggt gga tcc gga 307
 Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val Leu Gly Gly Ser Gly
 55 60 65
 aac ggc gag cag atc gcc gcc aac aag gtc aag ggt gca cgt tgt gca 355
 Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys Gly Ala Arg Cys Ala
 70 75 80 85
 ctt gct tgg tct gtt gaa act gca cgc ctc gcc cgc gag cac aac aat 403
 Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala Arg Glu His Asn Asn
 90 95 100
 gcg aac ctc atc ggc atc ggc ggc cgc atg cac tca gag 442
 Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His Ser Glu
 105 110

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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Gly Ala His Thr Tyr Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile
 35 40 45
 Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val
 50 55 60
 Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys
 65 70 75 80
 Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala
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 Arg Glu His Asn Asn Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His
 100 105 110
 Ser Glu

<210> 9
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<223> RXN01312

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 Met Ser Thr His Ser
 1 5

gaa acc acc cgc cca gag ttc atc cac cca gtc tca gtc ctc cca gag 163
 Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
 10 15 20

gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc 211
 Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
 25 30 35

acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259
 Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
 40 45 50

cca ctg aac cga cgc aag ttc cgt gtc ctc gtc gtt ggc acc ggc ctg 307
 Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
 55 60 65

tcc ggt ggt gct gca gca gca gcc ctc ggc gaa ctc gga tac gac gtc 355
 Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
 70 75 80 85

aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct 403
 Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
 90 95 100

gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac 451
 Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp
 105 110 115

ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt 499
 Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg
 120 125 130

ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc 547
 Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
 135 140 145

atc gac cac atg aac gcc atc ggt gca cca ttc gcc cgc gaa tac ggt 595
 Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
 150 155 160 165

ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc 643
 Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
 170 175 180

tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca 691
 Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
 185 190 195

tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc 739
 Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
 200 205 210

cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag	787
His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys	
215 220 225	
cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc	835
Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr	
230 235 240 245	
gca cac acc ggc cat gcc gtt atc ctg gca acc ggt ggc tac ggc aac	883
Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn	
250 255 260	
gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc	931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile	
265 270 275	
atg cgt gca tac gaa gcc ggc gca tac ttc gcg tcc cca tcg ttc atc	979
Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile	
280 285 290	
cag ttc cac cca acc ggc ctg cct gtg aac tcc acc tgg cag tcc aag	1027
Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys	
295 300 305	
acc att ctg atg tcc gag tcg ctg cgt aac gac ggc cgc atc tgg tcc	1075
Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser	
310 315 320 325	
cct aag gaa ccg aac gat aac cgc gat cca aac acc atc cct gag gat	1123
Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp	
330 335 340	
gag cgc gac tac ttc ctg gag cgc cgc tac cca gca ttc ggt aac ctc	1171
Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu	
345 350 355	
gtc cca cgt gac gtt gct tcc cgt gcg atc tcc cag cag atc aat gct	1219
Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala	
360 365 370	
ggt ctc ggt gtt gga cct ctg aac aac gct gca tac ctg gac ttc cgc	1267
Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg	
375 380 385	
gac gcc acc gag cgc ctc gga cag gac acc atc cgc gag cgt tac tcc	1315
Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser	
390 395 400 405	
aac ctc ttc acc atg tac gaa gag gca att ggc gag gac cca tac tcc	1363
Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser	
410 415 420	
agc cca atg cgt att gca ccg acc tgc cac ttc acc atg ggt ggc ctc	1411
Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu	
425 430 435	
tgg act gac ttc aac gaa atg acg tca ctc cca ggt ctg ttc tgc gca	1459
Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala	
440 445 450	

ggc gaa gca tcc tgg acc tac cac ggt gca aac cgt ctg ggc gca aac 1507
 Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn
 455 460 465

tcc ctg ctc tcc gct tcc gtc gat ggc tgg ttc acc ctg cca ttc acc 1555
 Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr
 470 475 480 485

atc cct aac tac ctc ggc cca ttg ctt ggc tcc gag cgt ctg tca gag 1603
 Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
 490 495 500

gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att 1651
 Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile
 505 510 515

gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac 1699
 Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
 520 525 530

gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc 1747
 Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
 535 540 545

tgt ggc gtt tcc cga aac gta gaa gac ctc cag gat ggc atc aac aag 1795
 Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys
 550 555 560 565

atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc 1843
 Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly
 570 575 580

agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc 1891
 Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala
 585 590 595

gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc 1939
 Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg
 600 605 610

gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat 1987
 Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp
 615 620 625

ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg 2035
 Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp
 630 635 640 645

gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc 2083
 Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe
 650 655 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact 2129
 Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr Lys
 665 670

tacacttgag atc 2142

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<211> 673

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
 35 40 45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
 50 55 60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu
 65 70 75 80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
 85 90 95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
 100 105 110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
 115 120 125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
 130 135 140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
 145 150 155 160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
 165 170 175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
 180 185 190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
 195 200 205

Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
 210 215 220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
 225 230 235 240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
 245 250 255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
 260 265 270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
 275 280 285

Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
 290 295 300

Thr Trp Gln Ser Lys Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp
 305 310 315 320
 Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
 325 330 335
 Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
 340 345 350
 Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
 355 360 365
 Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala
 370 375 380
 Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
 385 390 395 400
 Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
 405 410 415
 Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe
 420 425 430
 Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro
 435 440 445
 Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn
 450 455 460
 Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe
 465 470 475 480
 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
 485 490 495
 Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
 500 505 510
 Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
 515 520 525
 Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
 530 535 540
 Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln
 545 550 555 560
 Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn
 565 570 575
 Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr
 580 585 590
 Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
 595 600 605
 Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp
 610 615 620
 His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys

625		630		635		640
Phe Val Ser Ala Trp	Glu Pro Gly Glu	Asn Gly Thr Phe Val	Cys His			
	645	650	655			
Ala Glu Pro Leu Phe	Phe Glu Ser Val	Pro Leu Gln Thr	Arg Asn Tyr			
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Lys

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1077)
 <223> FRXA01312

<400> 11

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gat aac cgc gat cca aac acc atc cct gag gat gag cgc gac tac ttc	96
Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe	
20 25 30	
ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt	144
Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val	
35 40 45	
gct tcc cgt gcg atc tcc cag cag atc aat gct ggt ctc ggt gtt gga	192
Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly	
50 55 60	
cct ctg aac aac gct gca tac ctg gac ttc cgc gac gcc acc gag cgc	240
Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg	
65 70 75 80	
ctc gga cag gac acc atc cgc gag cgt tac tcc aac ctc ttc acc atg	288
Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met	
85 90 95	
tac gaa gag gca att ggc gag gac cca tac tcc agc cca atg cgt att	336
Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile	
100 105 110	
gca ccg acc tgc cac ttc acc atg ggt ggc ctc tgg act gac ttc aac	384
Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn	
115 120 125	
gaa atg acg tca ctc cca ggt ctg ttc tgc gca ggc gaa gca tcc tgg	432
Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp	
130 135 140	
acc tac cac ggt gca aac cgt ctg ggc gca aac tcc ctg ctc tcc gct	480
Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala	

145	150	155	160	
tcc gtc gat ggc tgg ttc acc ctg cca ttc acc atc cct aac tac ctc				528
Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu	165	170	175	
ggc cca ttg ctt ggc tcc gag cgt ctg tca gag gat gca cca gaa gca				576
Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala	180	185	190	
cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc				624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly	195	200	205	
aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac				672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr	210	215	220	
cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga				720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg	225	230	235	240
aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc				768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg	245	250	255	
gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg				816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met	260	265	270	
aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc				864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu	275	280	285	
ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc				912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly	290	295	300	
gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt				960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg	305	310	315	320
gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat				1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn	325	330	335	
gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca				1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro	340	345	350	
ctg cag aca agg aac tac aag taatgaaact tacacttgag atc				1100
Leu Gln Thr Arg Asn Tyr Lys	355			

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<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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 20 25 30
 Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
 35 40 45
 Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
 50 55 60
 Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
 65 70 75 80
 Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
 85 90 95
 Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
 100 105 110
 Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
 115 120 125
 Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
 130 135 140
 Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
 145 150 155 160
 Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
 165 170 175
 Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
 180 185 190
 Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
 195 200 205
 Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
 210 215 220
 His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
 225 230 235 240
 Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
 245 250 255
 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
 260 265 270
 Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
 275 280 285
 Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
 290 295 300
 Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
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 Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn

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<213> Corynebacterium glutamicum
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<223> RXN00231
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					Met	Thr	Ile	Asn	Val							
					1				5							
ttc	gaa	cta	ctt	gtc	aaa	agt	ccc	acg	ggc	cta	ctg	att	ggc	gat	tcc	163
Phe	Glu	Leu	Leu	Val	Lys	Ser	Pro	Thr	Gly	Leu	Leu	Ile	Gly	Asp	Ser	
				10					15					20		
tgg	gtg	gaa	gca	tcc	gac	ggc	ggc	act	ttc	gat	gtg	gaa	aac	cca	gcg	211
Trp	Val	Glu	Ala	Ser	Asp	Gly	Gly	Thr	Phe	Asp	Val	Glu	Asn	Pro	Ala	
			25					30					35			
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Thr	Gly	Glu	Thr	Ile	Ala	Thr	Leu	Ala	Ser	Ala	Thr	Ser	Glu	Asp	Ala	
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ctg	gct	gct	ctt	gat	gct	gca	tgc	gct	gtt	cag	gcc	gag	tgg	gct	agg	307
Leu	Ala	Ala	Leu	Asp	Ala	Ala	Cys	Ala	Val	Gln	Ala	Glu	Trp	Ala	Arg	
	55					60					65					
atg	cca	gcg	cgc	gag	cgt	tct	aat	att	tta	cgc	cgc	ggc	ttt	gag	ctc	355
Met	Pro	Ala	Arg	Glu	Arg	Ser	Asn	Ile	Leu	Arg	Arg	Gly	Phe	Glu	Leu	
70					75					80					85	
gta	gca	gaa	cgt	gca	gaa	gag	ttc	gcc	acc	ctc	atg	acc	ttg	gaa	atg	403
Val	Ala	Glu	Arg	Ala	Glu	Glu	Phe	Ala	Thr	Leu	Met	Thr	Leu	Glu	Met	
				90					95					100		
ggc	aag	cct	ttg	gct	gaa	gct	cgc	ggc	gaa	gtc	acc	tac	ggc	aac	gaa	451
Gly	Lys	Pro	Leu	Ala	Glu	Ala	Arg	Gly	Glu	Val	Thr	Tyr	Gly	Asn	Glu	
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ttc	ctg	cgc	tgg	ttc	tct	gag	gaa	gca	gtt	cgt	ctg	tat	ggc	cgt	tac	499
Phe	Leu	Arg	Trp	Phe	Ser	Glu	Glu	Ala	Val	Arg	Leu	Tyr	Gly	Arg	Tyr	
			120				125					130				
gga	acc	aca	cca	gaa	ggc	aac	ttg	cgg	atg	ctg	acc	gcc	ctc	aag	cca	547
Gly	Thr	Thr	Pro	Glu	Gly	Asn	Leu	Arg	Met	Leu	Thr	Ala	Leu	Lys	Pro	
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Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met	
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gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg	643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val	
170 175 180	
ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag	691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln	
185 190 195	
acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc	739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser	
200 205 210	
ggg gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc	787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg	
215 220 225	
ctt cgt aaa gtc tcc ttc acc ggc tcc acc cca gtt ggc cag cag ctg	835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu	
230 235 240 245	
ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt	883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly	
250 255 260	
ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg	931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala	
265 270 275	
atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc	979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys	
280 285 290	
acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc	1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe	
295 300 305	
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Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly	
310 315 320 325	
ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga	1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg	
330 335 340	
gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc	1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr	
345 350 355	
gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa	1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu	
360 365 370	
cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa	1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu	
375 380 385	

gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa 1315
 Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
 390 395 400 405

gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat 1363
 Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
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gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc 1411
 Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
 425 430 435

gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct 1459
 Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
 440 445 450

gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt 1507
 Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
 455 460 465

ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg 1555
 Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
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 Asp Pro Tyr Ala Gly
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<210> 14

<211> 490

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala
 35 40 45

Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
 50 55 60

Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65 70 75 80

Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu
 85 90 95

Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
 100 105 110

Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
 115 120 125

Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
 130 135 140

Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn
 145 150 155 160
 Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala
 165 170 175
 Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser
 180 185 190
 Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val
 195 200 205
 Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile
 210 215 220
 Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro
 225 230 235 240
 Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr
 245 250 255
 Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala
 260 265 270
 Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn
 275 280 285
 Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser
 290 295 300
 Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln
 305 310 315 320
 Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val
 325 330 335
 Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val
 340 345 350
 Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala
 355 360 365
 Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala
 370 375 380
 Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr
 385 390 395 400
 Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr
 405 410 415
 Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg
 420 425 430
 Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val
 435 440 445
 Ile Ser Asn Ala Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met
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Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
 485 490

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 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01311

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 Met Lys Leu Thr Leu
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 gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
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 gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35
 gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50
 ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65
 gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70 75 80 85
 cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403
 Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
 90 95 100
 ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451
 Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
 105 110 115
 tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499
 Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
 120 125 130
 gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
 135 140 145
 gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595

Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
 150 155 160 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
 170 175 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg 691
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
 185 190 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
 200 205 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
 215 220 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
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ggc aaa gac gac tagtctttaa tccaagtaag tac 870
 Gly Lys Asp Asp

<210> 16

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

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 20 25 30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
 35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
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Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
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Arg Ala Ala Phe Arg Gly Lys Asp Asp
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<210> 17
 <211> 1530
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01535

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 Met Thr Glu Gln Glu
 1 5

ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163
 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
 10 15 20

gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
 25 30 35

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
 Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
 40 45 50

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307
 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
 55 60 65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355
 Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
 70 75 80 85

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt 403
 Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly

90										95					100					
act	tcc	tcc	aac	atg	aac	acc	aat	gag	gtt	atc	gct	tcc	atc	gcg	aag	451				
Thr	Ser	Ser	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	Ala	Ser	Ile	Ala	Lys					
			105					110					115							
gct	aac	ggc	gtt	gag	gtt	cac	cca	aat	gac	cac	gtc	aac	atg	ggt	cag	499				
Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Gly	Gln					
		120					125					130								
tcc	tcc	aat	gac	acc	ttc	cct	act	gca	act	cac	gtt	gct	gca	acc	gaa	547				
Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His	Val	Ala	Ala	Thr	Glu					
		135				140					145									
gct	gct	gtc	aat	gac	ctc	atc	cca	ggc	ctg	aag	gtt	ctg	cac	gag	tct	595				
Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys	Val	Leu	His	Glu	Ser					
150					155					160					165					
ttg	gcg	aag	aag	gct	aac	gag	tgg	tct	gag	gtt	gtt	aag	tcc	ggc	cgc	643				
Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	Val	Lys	Ser	Gly	Arg					
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acc	cac	ctg	atg	gac	gct	gtt	cca	gta	acc	ctg	ggc	cag	gag	ttc	ggt	691				
Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly					
			185					190					195							
ggc	tac	gct	cgc	cag	atc	cag	ctc	ggc	atc	gag	cgc	gtt	gag	gct	act	739				
Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	Arg	Val	Glu	Ala	Thr					
		200					205					210								
ctt	cct	cgc	ctt	ggt	gag	ctg	gct	att	ggt	ggc	acc	gct	gct	ggt	acc	787				
Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr					
	215					220					225									
ggt	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	gtt	gtt	gct	gaa	ctg	835				
Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu					
230					235					240					245					
atc	aac	ttg	acc	gac	gtc	aag	gag	ctc	aag	gaa	gct	gag	aac	cac	ttc	883				
Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe					
				250					255					260						
gag	gct	cag	gct	gca	cgc	gac	gct	ctt	gtt	gag	ttc	tcc	ggc	gca	atg	931				
Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met					
			265					270					275							
cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979				
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu					
		280					285					290								
atg	ggc	tcc	ggc	cca	ctg	acc	ggt	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027				
Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	Asp					
		295				300					305									
ctg	cag	cca	ggt	tcc	tcc	atc	atg	cca	ggc	aag	gtc	aac	cca	gtt	ctc	1075				
Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Leu					
310					315					320					325					
tgt	gag	acc	gct	acc	cag	gtt	tcc	gct	cag	gtt	atc	ggc	aat	gac	gca	1123				
Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	Ile	Gly	Asn	Asp	Ala					
				330					335					340						

gct gtt gcg ttc tcc ggc acc cag ggc cag ttc gag ctc aac gtg ttc 1171
 Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe Glu Leu Asn Val Phe
 345 350 355
 atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct 1219
 Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
 360 365 370
 aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca 1267
 Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
 375 380 385
 aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt 1315
 Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
 390 395 400 405
 acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct 1363
 Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
 410 415 420
 aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat 1411
 Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
 425 430 435
 ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag 1459
 Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
 440 445 450
 cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507
 Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe
 455 460 465
 taaaactaga acccgataaa taa 1530

<210> 18
 <211> 469
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 18
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 Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg
 35 40 45
 Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
 50 55 60
 Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
 65 70 75 80
 Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
 85 90 95
 Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile

100	105	110
Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His Pro Asn Asp His 115	120	125
Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His 130	135	140
Val Ala Ala Thr Glu Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys 145	150	155
Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val 165	170	175
Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val Pro Val Thr Leu 180	185	190
Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu 195	200	205
Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly 210	215	220
Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys 225	230	235
Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu 245	250	255
Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu 260	265	270
Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala 275	280	285
Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu 290	295	300
Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys 305	310	315
Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val 325	330	335
Ile Gly Asn Asp Ala Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe 340	345	350
Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser 355	360	365
Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val 370	375	380
Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser 385	390	395
Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala 405	410	415
Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg 420	425	430

Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
 435 440 445

Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
 450 455 460

Arg Glu Asn Lys Phe
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<210> 19
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1141)
 <223> RXA00517

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 Met Pro Glu Val Thr
 1 5

gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa 163
 Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
 10 15 20

act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg 211
 Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
 25 30 35

cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct 259
 Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
 40 45 50

tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac 307
 Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
 55 60 65

gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac 355
 Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
 70 75 80 85

aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg 403
 Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
 90 95 100

act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc 451
 Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
 105 110 115

aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa 499
 Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg Lys Ala Ala Ala Gln
 120 125 130

gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc 547

Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser Pro Ala Met Ala Pro	
135 140 145	
tgg ggt ggc aga gaa aaa cgg atc ggt acc aac cca tgg tct att gcg	595
Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn Pro Trp Ser Ile Ala	
150 155 160 165	
gca cct ttt gga gaa acg gct acg gta gtc gat ata gcc aat act gcg	643
Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp Ile Ala Asn Thr Ala	
170 175 180	
gtt gcg cgc gga aag atc tac cac gca cga cag aca aac atg ccc att	691
Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln Thr Asn Met Pro Ile	
185 190 195	
cct gag act tgg gcg atc acg agt gag ggc gca ccc acc acg gat cct	739
Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala Pro Thr Thr Asp Pro	
200 205 210	
gct gag gca atc aac ggt gtc gtc ctt ccc atg gct ggt cac aaa ggt	787
Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met Ala Gly His Lys Gly	
215 220 225	
tat gcg att agc ttc atg atg gat gtg ctt tct gga gtt ctc act ggt	835
Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser Gly Val Leu Thr Gly	
230 235 240 245	
tcc cag cac agc acc aag gta cat ggt ccg tat gat ccc act ccc cca	883
Ser Gln His Ser Thr Lys Val His Gly Pro Tyr Asp Pro Thr Pro Pro	
250 255 260	
ggt gga gct ggc cac ttg ttc atc gcg ttg gat gtt gca gcg ttt cgc	931
Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp Val Ala Ala Phe Arg	
265 270 275	
gat cca caa gat ttc gat gac gca ctc agc gat ctg gtt ggg gaa gtt	979
Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp Leu Val Gly Glu Val	
280 285 290	
aaa tcc act ccg aaa gca caa aac acc gag gag att ttc tac ccc ggt	1027
Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu Ile Phe Tyr Pro Gly	
295 300 305	
gaa tcg gaa gac cgt gcg cat cgg aaa aac tct gcg cac ggt att tca	1075
Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser Ala His Gly Ile Ser	
310 315 320 325	
ttg cct gaa aaa acg tgg atg gaa ctg caa gaa ctg gca atc gag aac	1123
Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu Leu Ala Ile Glu Asn	
330 335 340	
cat gtt gta act cac cgt tgatctgcgc gttaaactcg gcc	1164
His Val Val Thr His Arg	
345	

<210> 20

<211> 347

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Met Pro Glu Val Thr Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr
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Asp Ile Leu Thr Lys Thr Gly Val Pro Ala Ala Asp Ala His Leu Val
 20 25 30

Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly
 35 40 45

Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met
 50 55 60

Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu
 65 70 75 80

Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala
 85 90 95

Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val
 100 105 110

Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg
 115 120 125

Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser
 130 135 140

Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn
 145 150 155 160

Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp
 165 170 175

Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln
 180 185 190

Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala
 195 200 205

Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met
 210 215 220

Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser
 225 230 235 240

Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr
 245 250 255

Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp
 260 265 270

Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp
 275 280 285

Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu
 290 295 300

Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
 305 310 315 320

Ala His Gly Ile Ser Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu
 325 330 335

Leu Ala Ile Glu Asn His Val Val Thr His Arg
 340 345

<210> 21
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1084)
 <223> RXA01350

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ggttccttaga ggacccccta caaggattga ggattgttta atg aat tcc ccg cag 115
 Met Asn Ser Pro Gln
 1 5

aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc 163
 Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
 10 15 20

tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa gta ttc ggc acc 211
 Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
 25 30 35

gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
 Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
 40 45 50

ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc 307
 Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
 55 60 65

ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc 355
 Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
 70 75 80 85

gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa 403
 Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
 90 95 100

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa 451
 Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
 105 110 115

ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt 499
 Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
 120 125 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc 547
 Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
 135 140 145

cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac 595

Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
 150 155 160 165

aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg 643
 Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
 170 175 180

gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc 691
 Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe
 185 190 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg 739
 Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
 200 205 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac 787
 Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
 215 220 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct 835
 Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
 230 235 240 245

gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc 883
 Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
 250 255 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att 931
 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
 265 270 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag 979
 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
 280 285 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc 1027
 Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
 295 300 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc 1075
 Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg
 310 315 320 325

gac ttg ctc taatctttaa cgc atg actt cgc 1107
 Asp Leu Leu

<210> 22

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile

35					40					45									
Pro	Gln	Ala	Leu	Gly	Gly	Ala	Glu	Gly	Val	Ala	Met	Glu	Leu	Leu	Asp				
50					55					60									
Ser	Ala	Phe	Pro	Leu	Leu	Arg	Asn	Ile	Thr	Ile	Thr	Ala	Asp	Ala	Asn				
65					70					75					80				
Glu	Ala	Phe	Asp	Gly	Ala	Asn	Ala	Ala	Phe	Leu	Val	Gly	Ala	Lys	Pro				
85					90					95									
Arg	Gly	Lys	Gly	Glu	Glu	Arg	Ala	Asp	Leu	Leu	Ala	Asn	Asn	Gly	Lys				
100					105					110									
Ile	Phe	Gly	Pro	Gln	Gly	Lys	Ala	Ile	Asn	Asp	Asn	Ala	Ala	Asp	Asp				
115					120					125									
Ile	Arg	Val	Leu	Val	Val	Gly	Asn	Pro	Ala	Asn	Thr	Asn	Ala	Leu	Ile				
130					135					140									
Ala	Ser	Ala	Ala	Ala	Pro	Asp	Val	Pro	Ala	Ser	Arg	Phe	Asn	Ala	Met				
145					150					155					160				
Met	Arg	Leu	Asp	His	Asn	Arg	Ala	Ile	Ser	Gln	Leu	Ala	Thr	Lys	Leu				
165					170					175									
Gly	Arg	Gly	Ser	Ala	Glu	Phe	Asn	Asn	Ile	Val	Val	Trp	Gly	Asn	His				
180					185					190									
Ser	Ala	Thr	Gln	Phe	Pro	Asp	Ile	Thr	Tyr	Ala	Thr	Val	Gly	Gly	Glu				
195					200					205									
Lys	Val	Thr	Asp	Leu	Val	Asp	His	Asp	Trp	Tyr	Val	Glu	Glu	Phe	Ile				
210					215					220									
Pro	Arg	Val	Ala	Asn	Arg	Gly	Ala	Glu	Ile	Ile	Glu	Val	Arg	Gly	Lys				
225					230					235					240				
Ser	Ser	Ala	Ala	Ser	Ala	Ala	Ser	Ser	Ala	Ile	Asp	His	Met	Arg	Asp				
245					250					255									
Trp	Val	Gln	Gly	Thr	Glu	Ala	Trp	Ser	Ser	Ala	Ala	Ile	Pro	Ser	Thr				
260					265					270									
Gly	Ala	Tyr	Gly	Ile	Pro	Glu	Gly	Ile	Phe	Val	Gly	Leu	Pro	Thr	Val				
275					280					285									
Ser	Arg	Asn	Gly	Glu	Trp	Glu	Ile	Val	Glu	Gly	Leu	Glu	Ile	Ser	Asp				
290					295					300									
Phe	Gln	Arg	Ala	Arg	Ile	Asp	Ala	Asn	Ala	Gln	Glu	Leu	Gln	Ala	Glu				
305					310					315					320				
Arg	Glu	Ala	Val	Arg	Asp	Leu	Leu												
325																			

<210> 23

<211> 1092

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1069)

<223> RXA02149

<400> 23

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                                     Met Pro Gln Lys Pro
                                     1 5

gcc agt ttc gcg gtg ggc ttt gac atc ggc ggc acc aac atg cga gcc 163
Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly Thr Asn Met Arg Ala
                10                15                20

ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tgc gcg ccg 211
Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
                25                30                35

tcg ccg cgc acg acg cag gca atg gaa cag ggg att ttt gat cta gtc 259
Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly Ile Phe Asp Leu Val
                40                45                50

gaa cag ctc aag gcc gaa tac ccg gtt ggt gct gtg gga ctt gcc gtc 307
Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val
                55                60                65

gcg gga ttt ttg gat cct gag tgc gag gtt gtt cga ttt gcc ccg cac 355
Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His
                70                75                80                85

ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg 403
Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu
                90                95                100

ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt 451
Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly
                105                110                115

gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg 499
Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
                120                125                130

gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att 547
Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
                135                140                145

tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt 595
Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
                150                155                160                165

gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag 643
Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
                170                175                180

cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct 691
Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala
                185                190                195

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tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc 739
 Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala
 200 205 210

gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa 787
 Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln
 215 220 225

gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg 835
 Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
 230 235 240 245

ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc 883
 Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
 250 255 260

atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc 931
 Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
 265 270 275

tcg gtc aac cac tat tcc acc cgc atc gtc ggc gca gga tat cgc cct 979
 Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro
 280 285 290

ttg gca cgc gtt gcc aca gct cag ttg ggt gcg gat gct ggc atg atc 1027
 Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala Asp Ala Gly Met Ile
 295 300 305

ggt gtc gct gat cta gct cga cgc tct gta gtg gaa gcc aac 1069
 Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val Glu Ala Asn
 310 315 320

taggtgtttt tcggtgggct gcg 1092

<210> 24

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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 20 25 30

Ser Leu Ser Ala Pro Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly
 35 40 45

Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala
 50 55 60

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
 65 70 75 80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
 85 90 95

Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
 100 105 110

Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
 115 120 125
 Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
 130 135 140
 Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
 145 150 155 160
 Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
 165 170 175
 Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
 180 185 190
 Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
 195 200 205
 Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
 210 215 220
 Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
 225 230 235 240
 Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
 245 250 255
 Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
 260 265 270
 Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
 275 280 285
 Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala
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 Asp Ala Gly Met Ile Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val
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 Glu Ala Asn

<210> 25
 <211> 1785
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1762)
 <223> RXA01814

<400> 25

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 Met Ala His Glu Arg

1

5

gcc ggg caa ctc gcc caa cca gaa gat ctc atc gat gtt gcg gaa ctg	163
Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu	
10 15 20	
gtc acc gca tat ttc acc cgc aag ccg gac gtg aac aac cct gat cag	211
Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln	
25 30 35	
cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc	259
Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser	
40 45 50	
gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac	307
Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp	
55 60 65	
tac cgc aac cag cag cca aaa aac tgg gtc ggc ccg ctg ttt atc ggc	355
Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly	
70 75 80 85	
cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag	403
Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu	
90 95 100	
gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc	451
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg	
105 110 115	
tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat	499
Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp	
120 125 130	
ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc	547
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly	
135 140 145	
atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa	595
Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys	
150 155 160 165	
tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg	643
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp	
170 175 180	
atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg	691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val	
185 190 195	
aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac	739
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr	
200 205 210	
gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc	787
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile	
215 220 225	
gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt	835
Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly	
230 235 240 245	
ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc	883

Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala	Glu	Thr	His	Gly	Leu	
				250					255					260		
aac	ctc	acc	gtg	gtc	aac	cca	cac	gtt	gat	tcc	acc	ttc	cgc	ttc	atg	931
Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	Thr	Phe	Arg	Phe	Met	
			265					270					275			
aca	ttg	gac	acc	gac	ggc	aag	atc	cgc	atg	gac	tgc	tcc	agc	cca	cac	979
Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp	Cys	Ser	Ser	Pro	His	
			280				285					290				
gca	atg	gca	tcg	ctg	att	gac	aac	cga	gac	aag	ttc	gat	gtg	gca	acc	1027
Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	Phe	Asp	Val	Ala	Thr	
	295					300					305					
ggc	aac	gac	gcc	gac	gcc	gac	cgc	cac	ggc	atc	gtc	acc	cca	gac	gct	1075
Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile	Val	Thr	Pro	Asp	Ala	
310				315						320				325		
ggc	ttg	atg	aac	ccc	aac	cac	tac	ctc	gca	gta	gca	att	gag	tac	ctc	1123
Gly	Leu	Met	Asn	Pro	Asn	His	Tyr	Leu	Ala	Val	Ala	Ile	Glu	Tyr	Leu	
			330						335					340		
ttt	gct	cac	cgc	cca	ggt	tgg	tcc	gca	gat	acc	gca	gtg	ggc	aaa	acc	1171
Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	Thr	
			345				350						355			
ctg	gtc	agc	tcc	tcc	atg	atc	gac	cgc	gtt	gtg	gcg	cag	ctt	ggc	cgc	1219
Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg	
			360				365					370				
acc	ctc	gtt	gag	gtt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggt	ttg	1267
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu	
	375					380					385					
atc	tcc	ggc	gaa	atc	gga	ttc	ggt	ggt	gaa	gaa	tcc	gca	ggt	gca	tcc	1315
Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser	
390				395					400					405		
ttc	ctc	cgc	atg	gac	ggc	acc	acc	tgg	tcc	acc	gac	aag	gac	ggc	ctc	1363
Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu	
			410					415					420			
atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr	
			425				430						435			
cca	tca	cag	cgc	tac	gca	gaa	ctc	gcc	gaa	gaa	ttc	ggt	gca	cct	gcc	1459
Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala	
			440				445					450				
tac	gcc	cgc	acc	gat	gca	gaa	gcc	aac	cga	gaa	caa	aag	gcc	atc	ctg	1507
Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu	
	455					460					465					
aag	gca	ctg	tcc	cca	gaa	cag	gtc	acc	gcc	acc	gaa	cta	gcc	ggc	gaa	1555
Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu	
470				475					480					485		
gca	atc	acc	gct	aag	ctc	acc	gaa	gct	ccc	ggc	aat	ggc	gca	gcc	atc	1603
Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly	Asn	Gly	Ala	Ala	Ile	

490	495	500	
gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca			1651
Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro			
505	510	515	
tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc			1699
Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly			
520	525	530	
gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc			1747
Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser			
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<212> PRT

<213> Corynebacterium glutamicum

<400> 26

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Asn	Asn	Pro	Asp	Gln	Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly
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Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr
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Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly
	65				70					75				80	

Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met
				85					90					95	

Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val
			100					105					110		

Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile
		115					120					125			

Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg
	130					135					140				

Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg
	145				150					155				160	

Asp	Gly	Gly	Phe	Lys	Tyr	Asn	Pro	Ala	Asn	Gly	Gly	Pro	Ala	Asp	Thr
				165					170					175	

Asp	Ala	Thr	Asp	Trp	Ile	Ala	Asn	Arg	Ala	Asn	Asp	Ile	Leu	Arg	Gly
				180				185					190		

Asp Leu Ala Asp Val Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu
 195 200 205
 Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro
 210 215 220
 Asn Val Val Asn Ile Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly
 225 230 235 240
 Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala
 245 250 255
 Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser
 260 265 270
 Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp
 275 280 285
 Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys
 290 295 300
 Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile
 305 310 315 320
 Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
 325 330 335
 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
 340 345 350
 Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
 355 360 365
 Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
 370 375 380
 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
 385 390 395 400
 Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
 405 410 415
 Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala
 420 425 430
 Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu
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 Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu
 450 455 460
 Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr
 465 470 475 480
 Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly
 485 490 495
 Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp
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 Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala

515

520

525

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<213> Corynebacterium glutamicum

<220>

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<222> (1)..(657)

<223> RXN02803

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 Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val
 20 25 30

gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct 144
 Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
 35 40 45

gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca 192
 Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
 50 55 60

ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt 240
 Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
 65 70 75 80

atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt 288
 Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
 85 90 95

gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg 336
 Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
 100 105 110

aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat 384
 Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
 115 120 125

gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct 432
 Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
 130 135 140

gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac 480
 Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
 145 150 155 160

atc aac atg gac tgc ggt tcc acc cac att gat cag gcg cag ccg cca 528

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
 165 170 175

gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct 576
 Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
 180 185 190

gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac 624
 Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
 195 200 205

caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa 677
 Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
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gaa 680

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 <213> Corynebacterium glutamicum

<400> 28
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Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
 35 40 45

Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
 50 55 60

Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
 65 70 75 80

Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
 85 90 95

Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
 100 105 110

Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
 115 120 125

Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
 130 135 140

Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
 145 150 155 160

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
 165 170 175

Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
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Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp

195

200

205

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 Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
 20 25 30
 ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca 144
 Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
 35 40 45
 tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt 192
 Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
 50 55 60
 gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg 240
 Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
 65 70 75 80
 gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc 288
 Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
 85 90 95
 atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag 336
 Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
 100 105 110
 gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca 384
 Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
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 Ala Asn Gly Ala Ala
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 <213> Corynebacterium glutamicum

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Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala	35	40	45
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly	50	55	60
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met	65	70	75
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val	85	90	95
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys	100	105	110
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala	115	120	125
Ala Asn Gly Ala Ala	130		

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 <223> RXN03076

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 Met Asp Glu Ser Arg
 1 5
 cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg 163
 Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
 10 15 20
 cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211
 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
 25 30 35
 gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259
 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
 40 45 50
 gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307
 Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
 55 60 65
 ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat 355

Gly 70	Pro	Leu	Arg	Val	Val 75	Val	Gly	Tyr	Asp	Ala 80	Arg	Tyr	Gly	Ser	His 85	
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Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala	Gly	Ala	Gly	Phe	Glu	
				90					95					100		
gtg	acg	ttg	ctc	ccc	acg	cct	agc	cct	acg	ccg	ttg	att	ccg	tgg	ttg	451
Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	Leu	Ile	Pro	Trp	Leu	
			105					110					115			
gtg	aac	aag	cat	ggg	ttg	gat	gcg	ggc	gtt	cag	atc	acg	gct	tcg	cat	499
Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln	Ile	Thr	Ala	Ser	His	
		120					125					130				
aat	ggt	gcg	gcg	gac	aat	ggc	tac	aag	gtg	ttt	ttg	tct	aat	ggt	cgc	547
Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	Leu	Ser	Asn	Gly	Arg	
	135					140					145					
cag	ctt	tat	tct	gaa	ctg	gag	cct	gag	ctt	gag	gcg	cat	atc	aat	gct	595
Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala	
150				155				160							165	
gtg	gaa	gat	ccg	att	cgg	gtt	cct	cgg	gtg	acg	gtg	cgc	ccc	act	gct	643
Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	Val	Arg	Pro	Thr	Ala	
				170				175						180		
gat	cag	ctg	cgt	cga	tat	gtt	gat	gag	atg	gtg	tcg	ttg	gtg	act	cct	691
Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	Ser	Leu	Val	Thr	Pro	
			185					190					195			
gat	cag	gct	gat	ttg	ttg	cgg	gtg	aat	tct	gag	cgg	ggc	aat	ctt	cgc	739
Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	Arg	Gly	Asn	Leu	Arg	
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Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	Arg	Ala	Met	Ala	Asn	
	215					220					225					
gct	ttc	caa	ttt	gct	ggg	ttt	ccc	cat	act	cat	ggc	gtg	aag	gct	cag	835
Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His	Gly	Val	Lys	Ala	Gln	
230				235						240					245	
cag	tat	cct	gat	ccc	acc	ttc	ccc	act	gtg	gcg	ttc	ccc	aat	ccg	gaa	883
Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu	
				250					255					260		
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn	
			265					270					275			
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val	
		280					285					290				
ggg	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu	
	295					300					305					
gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggg	gaa	1075
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu	

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ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg				1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu				
	330	335	340	
ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg				1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr				
	345	350	355	
gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt				1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu				
	360	365	370	
gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc				1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val				
	375	380	385	
gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg				1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp				
	390	395	400	405
gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat				1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn				
	410	415	420	
gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg				1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val				
	425	430	435	
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct				1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro				
	440	445	450	
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa				1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu				
	455	460	465	
aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt				1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg				
	470	475	480	485
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg				1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu				
	490	495	500	
gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat				1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His				
	505	510	515	
cag ctg gag gat gaa gtc caa agc tgg ttg agc aag ctt tagtttcctg				1700
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gctgctcccg gtt				1713

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<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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 20 25 30
 Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
 35 40 45
 Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
 50 55 60
 Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65 70 75 80
 Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
 85 90 95
 Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
 100 105 110
 Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
 115 120 125
 Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
 130 135 140
 Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
 145 150 155 160
 Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
 165 170 175
 Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
 180 185 190
 Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
 195 200 205
 Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
 210 215 220
 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
 225 230 235 240
 Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
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 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320

Glu	Tyr	Ser	Gly	Glu	Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	
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Ser	Ser	Gln	Leu	Leu	Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	
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Ser	Glu	Thr	Leu	Thr	Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	
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Leu	Asp	Gly	Pro	Leu	Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	
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Pro	Val	Pro	Asp	Val	Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	
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Phe	Met	Ala	Ser	Trp	Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu	
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Gln	Gln	Lys	Leu	Asn	Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser	
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Ser	Gln	Ile	Ala	Val	Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His	
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Trp	Ile	Ala	His	Pro	Gln	Gln	Glu	Leu	Ile	Gly	Val	Ser	Val	Thr	Pro	
				450						455		460				
His	Ile	Leu	Pro	Glu	Lys	Gln	Gly	Ile	Ala	Leu	His	Gly	Gln	Val	Gly	
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His	Val	His	Ile	Arg	Ala	Ile	Gly	Arg	Val	Ser	Gly	Thr	Glu	Ala	Lys	
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Ala	Lys	Leu	Tyr	Leu	Glu	Val	Gly	Gln	Ala	Ser	Ser	His	Asp	Glu	Ala	
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Ala	Gln	Leu	Leu	His	Gln	Leu	Glu	Asp	Glu	Val	Gln	Ser	Trp	Leu	Ser	
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Lys	Leu															
530																

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1684)
<223> FRXA02854
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                                     Met Asp Glu Ser Arg
                                     1         5

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Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala	
10 15 20	
cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt	211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val	
25 30 35	
gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg	259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu	
40 45 50	
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Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp	
55 60 65	
ggc ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat	355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His	
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Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu	
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Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu	
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Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His	
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aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc	547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg	
135 140 145	
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Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala	
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gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct	643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala	
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gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct	691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro	
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gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc	739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg	
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Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn	
215 220 225	
gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag	835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln	
230 235 240 245	
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Gln Tyr Pro Asp	Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu	
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Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg Ala Lys Glu Lys Asn		
265	270	275
gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg	979	
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val		
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ggc att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag	1027	
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu		
295	300	305
gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa	1075	
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu		
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Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu		
330	335	340
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Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr		
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Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val		
375	380	385
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Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp		
390	395	400
gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat	1363	
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn		
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Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val		
425	430	435
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct	1459	
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro		
440	445	450
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa	1507	
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu		
455	460	465
aaa cag ggc att gct ttg cat ggc cag gtg ggc cat gtg cat atc cgt	1555	
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg		
470	475	480
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg	1603	
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu		

	490	495	500	
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	Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His			
	505	510	515	
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	Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser			
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Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn				
35	40	45		
Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala				
50	55	60		
Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala				
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Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala				
85	90	95		
Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro				
100	105	110		
Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln				
115	120	125		
Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe				
130	135	140		
Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu				
145	150	155	160	
Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr				
165	170	175		
Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val				
180	185	190		
Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu				
195	200	205		
Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly				
210	215	220		
Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His				
225	230	235	240	

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320
 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
 325 330 335
 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
 340 345 350
 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
 355 360 365
 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
 370 375 380
 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
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<211> 536

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(513)

<223> RXA00511

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ttg aag att gct atg gat gaa gcc gga att aca ctg cgt acc acc aag 96
 Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
 20 25 30

gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc 144
 Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
 35 40 45

ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc 192
 Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60

act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct 240
 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80

gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg 288
 Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95

cca cag gtt ctg atc aat gtg cca gtt tcg gat aag tcc acc atc gtg 336
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110

agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg 384
 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt 432
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
 130 135 140

ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc 480
 Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
 145 150 155 160

gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533
 Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
 165 170

gca 536

<210> 36

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30
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 35 40 45
 Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60
 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80
 Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110
 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
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<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1474)

<223> RXN01365

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 Met Arg Thr Arg Glu
 1 5
 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20
 gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
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 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259

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Met	Arg	Asp	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Ala	Phe	Ala	Asp	Gly	Val		
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Thr	Ala	Gln	Gly	Leu	Asp	Val	Val	His	Leu	Gly	Leu	Thr	Ser	Thr	Asp		
		70			75				80						85		
gag	ctg	tac	ttt	gcg	tcc	gga	acc	ttg	aag	tgt	gct	ggg	gcg	atg	ttt	403	
Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys	Ala	Gly	Ala	Met	Phe		
				90					95					100			
act	gcg	tcg	cat	aac	ccc	gct	gag	tac	aac	ggc	atc	aag	ttg	tgt	cgt	451	
Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg		
			105					110					115				
gcg	ggg	gct	cgt	ccg	gtc	ggg	cag	gat	tct	ggg	ttg	gcc	aac	atc	att	499	
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
		120				125						130					
gat	gat	ctg	gtt	gag	ggg	gtt	cca	gcg	ttt	gat	ggg	gag	tca	ggg	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
		135				140					145						
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
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ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170					175					180			
gca	aac	ggc	atg	ggg	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggg	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
		200					205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
		215				220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggg	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
		230			235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250					255					260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
			265					270					275				
ccg	ggg	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		

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Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val Arg Thr Arg Val Gly			
295	300	305	
cac tcc ttc atc aag gcg aag atg gca gag acc ggt gcg gcc ttt ggt			1075
His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr Gly Ala Ala Phe Gly			
310	315	320	325
ggc gag cac tct gcg cac tac tac ttc act gag ttc ttc aat gcg gac			1123
Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu Phe Phe Asn Ala Asp			
330	335	340	
tcc ggc att ttg gct gcg atg cac gtg ctg gct gcg ctg gga agc cag			1171
Ser Gly Ile Leu Ala Ala Met His Val Leu Ala Ala Leu Gly Ser Gln			
345	350	355	
gac cag cca ctc agt gag atg atg gct agg tat aac cgg tac gtt gct			1219
Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr Asn Arg Tyr Val Ala			
360	365	370	
tca ggc gag ttg aac tcc cgt ttg gct aat gca gag gcg cag caa gag			1267
Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala Glu Ala Gln Gln Glu			
375	380	385	
cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg			1315
Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val			
390	395	400	405
gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg			1363
Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp			
410	415	420	
ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt			1411
Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val			
425	430	435	
gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta			1459
Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu			
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Gly Ile Ile Arg Ala			
455			

<210> 38

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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Arg	Gly	Val	Val	Gly	Val	Asp	Ile	Asp	Ala	Asp	Phe	Ile	Ser	Glu	Thr
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Gly	Ala	Ala	Phe	Gly	Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val
		35					40					45			

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
 290 295 300
 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
 305 310 315 320
 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
 325 330 335
 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
 340 345 350
 Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
 355 360 365

Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
 370 375 380

Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
 385 390 395 400

Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
 405 410 415

Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
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Leu Arg Leu Asn Val Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu
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Val Ala Glu Ile Leu Gly Ile Ile Arg Ala
 450 455

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 <213> Corynebacterium glutamicum

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 <223> FRXA01365

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 Met Arg Thr Arg Glu
 1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
 Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
 40 45 50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
 Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
 55 60 65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355
 Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
 70 75 80 85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403
 Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
 90 95 100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451

Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg		
			105					110					115				
gcg	ggt	gct	cgt	ccg	gtc	ggt	cag	gat	tct	ggt	ttg	gcc	aac	atc	att	499	
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
		120					125					130					
gat	gat	ctg	gtt	gag	ggt	gtt	cca	gcg	ttt	gat	ggt	gag	tca	ggt	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
		135				140					145						
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
150					155					160					165		
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
			170					175						180			
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
		185						190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
		200					205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
	215					220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
230					235					240				245			
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
			250					255						260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
		265					270						275				
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		
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gag	gtg	att	gct	gaa												994	
Glu	Val	Ile	Ala	Glu													
		295															

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<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
 20 25 30
 Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
 35 40 45
 Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
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 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
 290 295

<210> 41

<211> 1743

<212> DNA

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<220>

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<222> (101)..(1720)

<223> RXA00098

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				Met	Ala	Asp	Ile	Ser	
				1				5	

acc	acc	cag	gtt	tgg	caa	gac	ctg	acc	gat	cat	tac	tca	aac	ttc	cag	163
Thr	Thr	Gln	Val	Trp	Gln	Asp	Leu	Thr	Asp	His	Tyr	Ser	Asn	Phe	Gln	
			10						15					20		

gca	acc	act	ctg	cgt	gaa	ctt	ttc	aag	gaa	gaa	aac	cgc	gcc	gag	aag	211
Ala	Thr	Thr	Leu	Arg	Glu	Leu	Phe	Lys	Glu	Glu	Asn	Arg	Ala	Glu	Lys	
			25					30					35			

tac	acc	ttc	tcc	gcg	gct	ggc	ctc	cac	gtc	gac	ctg	tcg	aag	aat	ctg	259
Tyr	Thr	Phe	Ser	Ala	Ala	Gly	Leu	His	Val	Asp	Leu	Ser	Lys	Asn	Leu	
		40				45					50					

ctt	gac	gac	gcc	acc	ctc	acc	aag	ctc	ctt	gca	ctg	acc	gaa	gaa	tct	307
Leu	Asp	Asp	Ala	Thr	Leu	Thr	Lys	Leu	Leu	Ala	Leu	Thr	Glu	Glu	Ser	
	55					60				65						

ggc	ctt	cgc	gaa	cgc	att	gac	gcg	atg	ttt	gcc	ggt	gaa	cac	ctc	aac	355
Gly	Leu	Arg	Glu	Arg	Ile	Asp	Ala	Met	Phe	Ala	Gly	Glu	His	Leu	Asn	
70					75				80					85		

aac	acc	gaa	gac	cgc	gct	gtc	ctc	cac	acc	gcg	ctg	cgc	ctt	cct	gcc	403
Asn	Thr	Glu	Asp	Arg	Ala	Val	Leu	His	Thr	Ala	Leu	Arg	Leu	Pro	Ala	
			90					95						100		

gaa	gct	gat	ctg	tca	gta	gat	ggc	caa	gat	gtt	gct	gct	gat	gtc	cac	451
Glu	Ala	Asp	Leu	Ser	Val	Asp	Gly	Gln	Asp	Val	Ala	Ala	Asp	Val	His	
			105				110						115			

gaa	gtt	ttg	gga	cgc	atg	cgt	gac	ttc	gct	act	gcg	ctg	cgc	tca	ggc	499
Glu	Val	Leu	Gly	Arg	Met	Arg	Asp	Phe	Ala	Thr	Ala	Leu	Arg	Ser	Gly	
		120				125						130				

aac	tgg	ttg	gga	cac	acc	ggc	cac	acg	atc	aag	aag	atc	gtc	aac	att	547
Asn	Trp	Leu	Gly	His	Thr	Gly	His	Thr	Ile	Lys	Lys	Ile	Val	Asn	Ile	
	135					140					145					

ggt	atc	ggt	ggc	tct	gac	ctc	gga	cca	gcc	atg	gct	acg	aag	gct	ctg	595
Gly	Ile	Gly	Gly	Ser	Asp	Leu	Gly	Pro	Ala	Met	Ala	Thr	Lys	Ala	Leu	
150				155					160					165		

cgt	gca	tac	gcg	acc	gct	ggt	atc	tca	gca	gaa	ttc	gtc	tcc	aac	gtc	643
Arg	Ala	Tyr	Ala	Thr	Ala	Gly	Ile	Ser	Ala	Glu	Phe	Val	Ser	Asn	Val	
			170					175					180			

gac	cca	gca	gac	ctc	gtt	tct	gtg	ttg	gaa	gac	ctc	gat	gca	gaa	tcc	691
Asp	Pro	Ala	Asp	Leu	Val	Ser	Val	Leu	Glu	Asp	Leu	Asp	Ala	Glu	Ser	
			185					190					195			

aca	ttg	ttc	gtg	atc	gct	tcg	aaa	act	ttc	acc	acc	cag	gag	acg	ctg	739
Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr	Thr	Gln	Glu	Thr	Leu	

200					205					210						
tcc	aac	gct	cgt	gca	gct	cgt	gct	tgg	ctg	gta	gag	aag	ctc	ggt	gaa	787
Ser	Asn	Ala	Arg	Ala	Ala	Arg	Ala	Trp	Leu	Val	Glu	Lys	Leu	Gly	Glu	
215					220					225						
gag	gct	gtc	gcg	aag	cac	ttc	gtc	gca	gtg	tcc	acc	aat	gct	gaa	aag	835
Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser	Thr	Asn	Ala	Glu	Lys	
230					235					240					245	
gtc	gca	gag	ttc	ggg	atc	gac	acg	gac	aac	atg	ttc	ggc	ttc	tgg	gac	883
Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met	Phe	Gly	Phe	Trp	Asp	
250					255					260					265	
tgg	gtc	gga	ggg	cgt	tac	tcc	gtg	gac	tcc	gca	gtt	ggg	ctt	tcc	ctc	931
Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala	Val	Gly	Leu	Ser	Leu	
265					270					275					280	
atg	gca	gtg	atc	ggc	cct	cgc	gac	ttc	atg	cgt	ttc	ctc	ggg	gga	ttc	979
Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg	Phe	Leu	Gly	Gly	Phe	
280					285					290					295	
cac	gcg	atg	gat	gaa	cac	ttc	cgc	acc	acc	aag	ttc	gaa	gag	aac	gtt	1027
His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys	Phe	Glu	Glu	Asn	Val	
295					300					305					310	
cca	atc	ttg	atg	gct	ctg	ctc	ggg	gtc	tgg	tac	tcc	gat	ttc	tat	ggg	1075
Pro	Ile	Leu	Met	Ala	Leu	Leu	Gly	Val	Trp	Tyr	Ser	Asp	Phe	Tyr	Gly	
310					315					320					325	
gca	gaa	acc	cac	gct	gtc	cta	cct	tat	tcc	gag	gat	ctc	agc	cgt	ttt	1123
Ala	Glu	Thr	His	Ala	Val	Leu	Pro	Tyr	Ser	Glu	Asp	Leu	Ser	Arg	Phe	
330					335					340					345	
gct	gct	tac	ctc	cag	cag	ctg	acc	atg	gaa	tca	aat	ggc	aag	tca	gtc	1171
Ala	Ala	Tyr	Leu	Gln	Gln	Leu	Thr	Met	Glu	Ser	Asn	Gly	Lys	Ser	Val	
345					350					355					360	
cac	cgc	gac	ggc	tcc	cct	gtt	tcc	act	ggc	act	ggc	gaa	att	tac	tgg	1219
His	Arg	Asp	Gly	Ser	Pro	Val	Ser	Thr	Gly	Thr	Gly	Glu	Ile	Tyr	Trp	
360					365					370					375	
ggg	gag	cct	ggc	aca	aat	ggc	cag	cac	gct	ttc	ttc	cag	ctg	atc	cac	1267
Gly	Glu	Pro	Gly	Thr	Asn	Gly	Gln	His	Ala	Phe	Phe	Gln	Leu	Ile	His	
375					380					385					390	
cag	ggc	act	cgc	ctt	gtt	cca	gct	gat	ttc	att	ggg	ttc	gct	cgt	cca	1315
Gln	Gly	Thr	Arg	Leu	Val	Pro	Ala	Asp	Phe	Ile	Gly	Phe	Ala	Arg	Pro	
390					395					400					405	
aag	cag	gat	ctt	cct	gcc	ggg	gag	cgc	acc	atg	cat	gac	ctt	ttg	atg	1363
Lys	Gln	Asp	Leu	Pro	Ala	Gly	Glu	Arg	Thr	Met	His	Asp	Leu	Leu	Met	
410					415					420					425	
agc	aac	ttc	ttc	gca	cag	acc	aag	gtt	ttg	gct	ttc	ggg	aag	aac	gct	1411
Ser	Asn	Phe	Phe	Ala	Gln	Thr	Lys	Val	Leu	Ala	Phe	Gly	Lys	Asn	Ala	
425					430					435					440	
gaa	gag	atc	gct	gcg	gaa	ggg	gtc	gca	cct	gag	ctg	gtc	aac	cac	aag	1459
Glu	Glu	Ile	Ala	Ala	Glu	Gly	Val	Ala	Pro	Glu	Leu	Val	Asn	His	Lys	
440					445					450					455	

gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt 1507
 Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
 455 460 465

acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg 1555
 Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
 470 475 480 485

atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt 1603
 Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
 490 495 500

gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct 1651
 Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
 505 510 515

ggc gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att 1699
 Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
 520 525 530

aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag 1743
 Lys Trp Tyr Arg Ala Asn Arg
 535 540

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<211> 540

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
 20 25 30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
 35 40 45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
 115 120 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
 130 135 140

Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
 145 150 155 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
165 170 175

Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
180 185 190

Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
195 200 205

Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
210 215 220

Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
225 230 235 240

Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
245 250 255

Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
260 265 270

Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
275 280 285

Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
290 295 300

Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
305 310 315 320

Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
325 330 335

Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
340 345 350

Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
355 360 365

Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
370 375 380

Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
385 390 395 400

Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
405 410 415

His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
420 425 430

Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
435 440 445

Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
450 455 460

Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
465 470 475 480

Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
 485 490 495

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
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Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
 515 520 525

Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
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 <222> (1)..(630)
 <223> RXA01989

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 Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
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 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30

ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat 144
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45

gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca 192
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60

gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct 240
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80

gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag 288
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95

tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct 336
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110

aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa 384
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata 432
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140

ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca 480

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga 528
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga 576
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190
 att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa 624
 Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205
 tta tct 630
 Leu Ser
 210

<210> 44
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 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 44
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 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140
 Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205

Leu Ser
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<210> 45
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 <212> DNA
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<220>
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 <222> (101)..(1246)
 <223> RXA00340

<400> 45
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ctcttacctc atcactgaca tctcttagaa agaccaccca gtg aaa tta gtc atc 115
 Val Lys Leu Val Ile
 1 5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc 163
 Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
 10 15 20

acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc 211
 Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
 25 30 35

tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga 259
 Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
 40 45 50

cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg 307
 Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
 55 60 65

gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg 355
 Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
 70 75 80 85

tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag 403
 Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
 90 95 100

gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt 451
 Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
 105 110 115

gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct 499
 Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
 120 125 130

gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta 547
 Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
 135 140 145

tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc	595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
150 155 160 165	
acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act	643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa	739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
230 235 240 245	
gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc	883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile	
250 255 260	
gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac	931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His	
265 270 275	
gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta	979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val	
280 285 290	
gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa	1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys	
295 300 305	
aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg	1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu	
310 315 320 325	
gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg	1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu	
330 335 340	
gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg	1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser	
345 350 355	
ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg	1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu	
360 365 370	
ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag	1266
Phe Asn Asp Thr Ser His Leu Glu Ala	
375 380	
ctc	1269

<210> 46
 <211> 382
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 46

Val	Lys	Leu	Val	Ile	Glu	Ala	Asp	Gly	Gly	Ser	Arg	Gly	Asn	Pro	Gly
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Val	Ala	Gly	Ser	Gly	Thr	Val	Val	Tyr	Ser	Asp	Asn	Lys	Ala	Glu	Val
			20					25					30		
Leu	Lys	Glu	Ile	Ala	Tyr	Val	Val	Gly	Thr	Lys	Ala	Thr	Asn	Asn	Val
		35					40					45			
Ala	Glu	Tyr	Arg	Gly	Leu	Leu	Glu	Gly	Leu	Lys	Ala	Ala	Arg	Glu	Leu
	50					55					60				
Gly	Ala	Thr	Ser	Val	Asp	Val	Tyr	Met	Asp	Ser	Lys	Leu	Val	Val	Glu
65					70				75						80
Gln	Met	Ser	Gly	Arg	Trp	Lys	Ile	Lys	His	Pro	Asp	Met	Lys	Val	Leu
				85					90					95	
Ala	Ile	Glu	Ala	Lys	Glu	Ile	Ala	Ser	Glu	Ile	Gly	Ser	Val	Ser	Tyr
			100					105					110		
Thr	Trp	Ile	Pro	Arg	Glu	Lys	Asn	Lys	Arg	Ala	Asp	Ala	Leu	Ser	Asn
		115					120					125			
Val	Ala	Met	Asp	Ala	Ala	Ala	Ala	Gly	Lys	Pro	Val	Gly	Val	Val	Gly
	130					135					140				
Asp	Ser	Ala	Ser	Val	Ser	Ser	Ala	Ser	Ser	Val	Ala	Gly	Ser	Glu	Lys
145					150					155					160
Glu	Asp	Leu	Asn	Cys	Thr	Glu	Thr	Lys	Pro	Thr	Asn	Trp	Asn	Gly	Ala
			165						170					175	
Thr	Thr	Asp	Pro	Thr	Arg	Phe	Leu	Leu	Leu	Arg	His	Gly	Gln	Thr	Ala
			180				185						190		
Met	Ser	Val	Ala	Arg	Leu	Tyr	Ser	Gly	Arg	Ser	Asn	Pro	Glu	Leu	Ser
		195					200					205			
Glu	Leu	Gly	Glu	Lys	Gln	Ala	Ala	Ala	Ala	Ala	Arg	Arg	Leu	Ala	Gln
	210					215					220				
Thr	Gly	Gly	Ile	Asp	Ala	Ile	Val	Ser	Ser	Pro	Leu	Thr	Arg	Thr	Met
225					230					235					240
Gln	Thr	Ala	Glu	Ala	Ala	Ala	Ala	Ala	Leu	Gly	Met	Lys	Val	Arg	Val
			245						250					255	
Ile	Asp	Asp	Leu	Ile	Glu	Thr	Asp	Phe	Gly	Leu	Trp	Asp	Gly	Lys	Ser
			260					265					270		
Phe	Ser	Glu	Ala	His	Glu	Gln	Asp	Pro	Glu	Leu	His	Thr	Lys	Trp	Leu
		275					280					285			

Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
290 295 300

Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
305 310 315 320

Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
325 330 335

Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
340 345 350

Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro
355 360 365

Thr Cys Val Arg Leu Phe Asn Asp Thr Ser His Leu Glu Ala
370 375 380

<210> 47

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXA02492

<400> 47

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aaacgcgcgt cgtggaacat aaagtggcaa actagtagcct atg act aac gga aaa 115
Met Thr Asn Gly Lys
1 5
ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
10 15 20
ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211
Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
25 30 35
gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
40 45 50
gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
55 60 65
atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
70 75 80 85
ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
90 95 100

cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
 Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
 105 110 115
 gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
 Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
 120 125 130
 ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
 Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
 135 140 145
 ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
 Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
 150 155 160 165
 gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
 Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
 170 175 180
 aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
 Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
 185 190 195
 cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta 739
 Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
 200 205 210
 gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc 787
 Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
 215 220 225
 gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca 837
 Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
 230 235
 ctc 840

<210> 48

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
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 Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
 20 25 30
 Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
 35 40 45
 Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
 50 55 60
 Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65 70 75 80
 Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu

				85					90					95					
Lys	Tyr	Gly	Asp	Asp	Gln	Phe	Met	Glu	Trp	Arg	Arg	Ser	Tyr	Asp	Thr				
			100					105					110						
Pro	Pro	Pro	Glu	Leu	Ala	Asp	Asp	Ala	Glu	Tyr	Ser	Gln	Ala	Asn	Asp				
		115					120					125							
Pro	Arg	Tyr	Ala	Asp	Leu	Asp	Val	Val	Pro	Arg	Thr	Glu	Cys	Leu	Lys				
	130					135					140								
Asp	Val	Val	Val	Arg	Phe	Val	Pro	Tyr	Phe	Glu	Glu	Glu	Ile	Leu	Pro				
145					150					155					160				
Arg	Ala	Lys	Lys	Gly	Glu	Thr	Val	Leu	Ile	Ala	Ala	His	Gly	Asn	Ser				
				165					170					175					
Leu	Arg	Ala	Leu	Val	Lys	His	Leu	Asp	Gly	Ile	Ser	Asp	Ala	Asp	Ile				
			180					185					190						
Ala	Glu	Leu	Asn	Ile	Pro	Thr	Gly	Ile	Pro	Leu	Val	Tyr	Glu	Ile	Ala				
		195					200					205							
Glu	Asp	Gly	Ser	Val	Val	Asn	Pro	Gly	Gly	Thr	Tyr	Leu	Asp	Pro	Glu				
	210					215					220								
Ala	Ala	Ala	Ala	Gly	Ala	Ala	Ala	Val	Ala	Asn	Gln	Gly	Asn	Lys					
225					230					235									

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<211> 729
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(706)  
<223> RXA00381
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Met Thr Gln Thr Ile
1 5

gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg 163
Val His Leu Val Arg His Gly Glu Val His Asn Pro Glu Lys Ile Leu
10 15 20

tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa 211
Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln
25 30 35

gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att 259
Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His Asp Val Thr Tyr Ile
40 45 50

gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc 307
Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr Ser Glu Pro Phe Ile

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55 60 65

aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca 355
 Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala
 70 75 80 85

ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg 403
 Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu
 90 95 100

tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc 451
 Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser
 105 110 115

tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg 499
 Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val
 120 125 130

gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc 547
 Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr
 135 140 145

cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc 595
 His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser
 150 155 160 165

ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca 643
 Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr
 170 175 180

tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa 691
 Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu
 185 190 195

cca gct cag gag att tgatcactcg tgcgtttgac caa 729
 Pro Ala Gln Glu Ile
 200

<210> 50

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
 1 5 10 15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
 20 25 30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
 35 40 45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
 50 55 60

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu
 65 70 75 80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly

85										90					95				
Trp	Arg	Ser	Gln	Leu	Trp	Asn	Pro	Val	Arg	Trp	Pro	Leu	Met	Tyr	Asn				
			100					105					110						
Pro	Thr	Leu	Pro	Ser	Trp	Gly	Glu	His	Tyr	Thr	Asp	Ile	Leu	Glu	Arg				
		115					120					125							
Met	Met	Ala	Ala	Val	Glu	Arg	Ala	Arg	Val	Ala	Ala	Glu	Gly	His	Glu				
		130				135					140								
Ala	Ile	Leu	Val	Thr	His	Gln	Leu	Pro	Ile	Val	Cys	Val	Gln	Arg	His				
145					150				155						160				
Ala	Arg	Gly	Gln	Ser	Leu	Ser	His	Asn	Pro	Ala	Thr	Arg	Gln	Cys	Asp				
				165				170						175					
Leu	Ala	Ser	Val	Thr	Ser	Leu	Val	Phe	Gln	Asp	Asp	Gln	Ile	Val	Gly				
			180					185					190						
Val	His	Tyr	Asn	Glu	Pro	Ala	Gln	Glu	Ile										
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<210> 51

<211> 822

<212> DNA

<213> Corynebacterium glutamicum .

<220>

<221> CDS

<222> (101)..(799)

<223> RXA02122

<400> 51

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ccttttttta	agtggg	cgggt	cagga	atattt	tcgcac	aggt	atg	ctg	cat	gtc	atg	115
							Met	Leu	His	Val	Met	
							1				5	

aag	ccg	ggt	tca	cac	gca	gct	gcc	gaa	aag	act	caa	tcc	act	gtg	gtt	163
Lys	Pro	Gly	Ser	His	Ala	Ala	Ala	Glu	Lys	Thr	Gln	Ser	Thr	Val	Val	
			10					15						20		

tta	ctc	att	cgg	cat	ggg	caa	acc	cca	aca	act	ggt	cag	gtt	ctg	cct	211
Leu	Leu	Ile	Arg	His	Gly	Gln	Thr	Pro	Thr	Thr	Gly	Gln	Val	Leu	Pro	
			25					30					35			

ggt	cag	acg	ccg	ggt	tta	cac	ctg	tct	gat	aag	ggt	gaa	gag	cag	gcg	259
Gly	Gln	Thr	Pro	Gly	Leu	His	Leu	Ser	Asp	Lys	Gly	Glu	Glu	Gln	Ala	
		40					45					50				

cgg	gag	gtg	gca	cag	cgt	ctg	gcg	gag	gtg	ccg	att	acc	gct	gtg	tat	307
Arg	Glu	Val	Ala	Gln	Arg	Leu	Ala	Glu	Val	Pro	Ile	Thr	Ala	Val	Tyr	
		55				60					65					

tca	tcg	ccg	atg	gag	cgt	gcg	cag	gaa	aca	gca	gca	ccg	acg	gtc	agc	355
Ser	Ser	Pro	Met	Glu	Arg	Ala	Gln	Glu	Thr	Ala	Ala	Pro	Thr	Val	Ser	
70					75					80					85	

gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat 403
 Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
 90 95 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag 451
 Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
 105 110 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt 499
 Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
 120 125 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc 547
 Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
 135 140 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat 595
 Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
 150 155 160 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg 643
 Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
 170 175 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
 185 190 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
 200 205 210

aat tcc aga aca gga tgc ttg gga tac ctt cga gac aaa ctt ccg aaa 787
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
 215 220 225

gct ccg caa cca tgatcacctc accatttgag cgc 822
 Ala Pro Gln Pro
 230

<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
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Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
 20 25 30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
 35 40 45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
 50 55 60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65 70 75 80

Ala	Pro	Thr	Val	Ser 85	Ala	His	Gly	Leu	Glu	Leu	Thr	Val	Glu	Pro	Gly
Leu	Ile	Glu	Cys 100	Asp	Phe	Gly	Glu	Trp 105	Thr	Gly	Arg	Lys	Leu	Thr	Glu
Leu	Asn	Ala 115	Leu	Glu	Glu	Trp	Lys 120	Ala	Val	Gln	Lys	Thr 125	Pro	Ser	Thr
Phe	Arg 130	Phe	Pro	Gly	Gly	Glu 135	Ser	Phe	Val	Glu	Met 140	Gln	Asp	Arg	Met
Val 145	Glu	Ala	Ile	Gly 150	Asn	Ile	Ala	Gln	Gln	His 155	Pro	Gly	Glu	Ile	Val 160
Ala	Ala	Phe	Ser	His 165	Ala	Asp	Thr	Ile	Lys 170	Ala	Ala	Val	Ala	His 175	Phe
Val	Gly	Thr	Pro 180	Leu	Asp	Ser	Phe	Gln 185	Arg	Ile	Phe	Ile	Asp 190	Thr	Ala
Ser	Ile	Ser 195	Ala	Val	Glu	Phe	Thr 200	Gly	Lys	Ser	Ser	Gly 205	Val	Ser	Ser
His 210	Met	Leu	Leu	Thr	Asn	Ser 215	Arg	Thr	Gly	Ser	Leu 220	Gly	Tyr	Leu	Arg
Asp 225	Lys	Leu	Pro	Lys	Ala 230	Pro	Gln	Pro							

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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00206
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Met Glu Asp Met Arg
1 5
att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc 163
Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
10 15 20
atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
25 30 35
gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta 259
Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
40 45 50

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Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly	
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acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga	355
Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly	
70 75 80 85	
att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt	403
Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu	
90 95 100	
atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct	451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser	
105 110 115	
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Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp	
120 125 130	
gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg	547
Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val	
135 140 145	
gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac	595
Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn	
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Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala	
170 175 180	
ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa	691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu	
185 190 195	
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Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe	
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Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu	
215 220 225	
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Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe	
230 235 240 245	
ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc	883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile	
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cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att	931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile	
265 270 275	
caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt	979
Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg	
280 285 290	
tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag	1027

Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
 310 315 320 325

gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
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<211> 346

<212> PRT

<213> *Corynebacterium glutamicum*

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Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
 35 40 45

Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80

Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110

Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140

Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
 145 150 155 160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190

Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
 195 200 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220

Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
 225 230 235 240

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
 305 310 315 320

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 325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1060)
 <223> RXA01243

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 Met Ile Leu Thr Val
 1 5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
 10 15 20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
 25 30 35

ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
 40 45 50

act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307
 Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
 55 60 65

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Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro	
70 75 80 85	
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Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys	
90 95 100	
ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt	451
Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu	
105 110 115	
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Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu	
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Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val	
135 140 145	
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Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala	
150 155 160 165	
gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg	643
Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr	
170 175 180	
tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act	691
Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr	
185 190 195	
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Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu	
200 205 210	
tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc	787
Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr	
215 220 225	
gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag	835
Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu	
230 235 240 245	
tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc	883
Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly	
250 255 260	
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Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn	
265 270 275	
gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc	979
Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala	
280 285 290	
aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag	1027
Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys	
295 300 305	
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310 315 320

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1083

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<212> PRT
<213> Corynebacterium glutamicum

<400> 56
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35 40 45
Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
50 55 60
His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
65 70 75 80
Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
85 90 95
Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
100 105 110
Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
115 120 125
Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
130 135 140
Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
145 150 155 160
Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
165 170 175
Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
180 185 190
Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
195 200 205
Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
210 215 220
Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
225 230 235 240
Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
245 250 255
Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe

260	265	270
Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn		
275	280	285
Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile		
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Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu		
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 <211> 1113
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1090)
 <223> RXA01882

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 Met Ile Ile Thr Phe
 1 5
 acc cca aac ccg agt att gat tcc acg ctg tgc ctc ggc gaa gag ctc 163
 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
 10 15 20
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 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
 25 30 35
 ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa 259
 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
 40 45 50
 acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
 Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
 55 60 65
 gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355
 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
 70 75 80 85
 gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403
 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
 90 95 100
 ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451
 Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
 105 110 115
 gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc 499

Glu	Lys	Val	Leu	Ile	Asp	Ala	Leu	Arg	Pro	Glu	Val	Thr	Trp	Val	Val		
		120						125					130				
ctg	gcg	ggc	tcg	ctg	cca	cca	ggg	gca	cca	gtt	gac	tgg	tac	gcg	cgt	547	
Leu	Ala	Gly	Ser	Leu	Pro	Pro	Gly	Ala	Pro	Val	Asp	Trp	Tyr	Ala	Arg		
		135					140				145						
ctc	acc	gcg	ttg	atc	cat	tca	gca	cgc	cct	gac	gtt	cgc	gtg	gct	gtc	595	
Leu	Thr	Ala	Leu	Ile	His	Ser	Ala	Arg	Pro	Asp	Val	Arg	Val	Ala	Val		
		150				155				160					165		
gat	acc	tca	gac	aag	cca	ctg	atg	gcg	ttg	ggc	gag	agc	ttg	gat	aca	643	
Asp	Thr	Ser	Asp	Lys	Pro	Leu	Met	Ala	Leu	Gly	Glu	Ser	Leu	Asp	Thr		
				170					175						180		
cct	ggc	gct	gct	ccg	aac	ctg	att	aag	cca	aat	ggg	ctg	gaa	ctg	ggc	691	
Pro	Gly	Ala	Ala	Pro	Asn	Leu	Ile	Lys	Pro	Asn	Gly	Leu	Glu	Leu	Gly		
			185					190					195				
cag	ctg	gct	aac	act	gat	ggg	gaa	gag	ctg	gag	gag	cgt	gct	gag	caa	739	
Gln	Leu	Ala	Asn	Thr	Asp	Gly	Glu	Glu	Leu	Glu	Ala	Arg	Ala	Ala	Gln		
		200					205					210					
ggc	gat	tac	gac	gcc	atc	atc	gca	gct	gag	gac	gta	ctg	gtt	aac	cgt	787	
Gly	Asp	Tyr	Asp	Ala	Ile	Ile	Ala	Ala	Ala	Asp	Val	Leu	Val	Asn	Arg		
		215				220					225						
ggc	atc	gaa	cag	gtg	ctt	gtc	acc	ttg	ggg	gcc	gca	gga	gag	gtg	ttg	835	
Gly	Ile	Glu	Gln	Val	Leu	Val	Thr	Leu	Gly	Ala	Ala	Gly	Ala	Val	Leu		
		230				235				240					245		
gtc	aac	gca	gaa	ggg	gag	tgg	act	gct	act	tct	cca	aag	att	gat	gtt	883	
Val	Asn	Ala	Glu	Gly	Ala	Trp	Thr	Ala	Thr	Ser	Pro	Lys	Ile	Asp	Val		
				250					255						260		
gta	tcc	acc	gtt	gga	gct	gga	gac	tgt	gct	ctt	gca	ggg	ttt	gtt	atg	931	
Val	Ser	Thr	Val	Gly	Ala	Gly	Asp	Cys	Ala	Leu	Ala	Gly	Phe	Val	Met		
			265					270						275			
gca	cgt	tcc	cag	aag	aaa	aca	ctg	gag	gaa	tct	ctg	ctg	aat	gcc	gtg	979	
Ala	Arg	Ser	Gln	Lys	Lys	Thr	Leu	Glu	Glu	Ser	Leu	Leu	Asn	Ala	Val		
		280					285					290					
tct	tac	ggc	tcg	act	gag	gag	tct	ctt	cct	ggc	act	acc	att	cct	cgt	1027	
Ser	Tyr	Gly	Ser	Thr	Ala	Ala	Ser	Leu	Pro	Gly	Thr	Thr	Ile	Pro	Arg		
		295				300					305						
cct	gac	caa	ctc	gcc	aca	gct	ggg	gca	acg	gtc	acc	caa	gtc	aaa	gga	1075	
Pro	Asp	Gln	Leu	Ala	Thr	Ala	Gly	Ala	Thr	Val	Thr	Gln	Val	Lys	Gly		
		310				315				320					325		
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Leu	Lys	Glu	Ser	Ala													
				330													

<210> 58

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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 35 40 45
 Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
 50 55 60
 Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
 65 70 75 80
 Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
 85 90 95
 Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
 100 105 110
 Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
 115 120 125
 Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
 130 135 140
 Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
 145 150 155 160
 Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
 165 170 175
 Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
 180 185 190
 Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
 195 200 205
 Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
 210 215 220
 Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
 225 230 235 240
 Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
 245 250 255
 Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
 260 265 270
 Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
 275 280 285
 Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
 290 295 300
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325 330

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<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1132)
<223> RXA01702

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Met Pro Ile Ala Thr
1 5
ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc 163
Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
10 15 20
gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct 211
Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
25 30 35
ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc 259
Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
40 45 50
acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc 307
Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
55 60 65
aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc 355
Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
70 75 80 85
tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc 403
Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
90 95 100
ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc 451
Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
105 110 115
gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc 499
Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
120 125 130
gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct 547
Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
135 140 145
aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc 595
Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
150 155 160 165

ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac 643
 Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
 170 175 180

acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt 691
 Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
 185 190 195

gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc 739
 Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
 200 205 210

gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag 787
 Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
 215 220 225

ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt 835
 Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
 230 235 240 245

cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag 883
 Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
 250 255 260

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
 265 270 275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
 280 285 290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
 295 300 305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
 310 315 320 325

gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123
 Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr
 330 335 340

acc tct aag taatctcagc agttaaaaag ggc 1155
 Thr Ser Lys

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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 20 25 30

Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
 35 40 45
 Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
 50 55 60
 Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
 65 70 75 80
 Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
 85 90 95
 Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
 100 105 110
 Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
 115 120 125
 Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
 130 135 140
 Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
 145 150 155 160
 Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
 165 170 175
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
 180 185 190
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
 195 200 205
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
 210 215 220
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
 225 230 235 240
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
 245 250 255
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
 260 265 270
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
 275 280 285
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
 290 295 300
 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
 305 310 315 320
 Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
 325 330 335
 Ser Val Gly Lys Thr Thr Ser Lys
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(877)
 <223> RXA02258

<400> 61

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 Met Ala Arg Lys Pro
 1 5

ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc 163
 Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile
 10 15 20

ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag 211
 Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu
 25 30 35

aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc 259
 Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val
 40 45 50

cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag 307
 Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln
 55 60 65

gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca 355
 Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala
 70 75 80 85

agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc 403
 Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser
 90 95 100

gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag 451
 Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys
 105 110 115

gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt 499
 Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly
 120 125 130

gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc 547
 Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val
 135 140 145

gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc 595
 Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala
 150 155 160 165

aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag 643
 Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys
 170 175 180

gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt 691
 Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly
 185 190 195

ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att 739
 Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
 200 205 210

ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt 787
 Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
 215 220 225

cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt 835
 Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
 230 235 240 245

gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct 877
 Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala
 250 255

taaagtacag agctttaag cac 900

<210> 62
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 62
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His Gln Gln Ala Ile Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro
 20 25 30

Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
 35 40 45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
 50 55 60

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
 65 70 75 80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
 85 90 95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
 100 105 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
 115 120 125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
 130 135 140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
 145 150 155 160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
 165 170 175

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
 180 185 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
 210 215 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
 225 230 235 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala
 245 250 255

Ser Val Ala

<210> 63
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1540)
 <223> RXN01225

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 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa	451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu	
105 110 115	
acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc	499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
120 125 130	
ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac	547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
135 140 145	
ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac	595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
150 155 160 165	
ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga	643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
170 175 180	
ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc	691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
185 190 195	
aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att	739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
200 205 210	
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc	787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
215 220 225	
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag	835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
230 235 240 245	
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag	883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
250 255 260	
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag	931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc	979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
280 285 290	
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc	1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
295 300 305	
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag	1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
310 315 320 325	
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa	1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu	
330 335 340	
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc	1171

Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
 345 350 355
 aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg 1219
 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
 gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
 atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
 gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480
 cac 1563

<210> 64

<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

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 Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
 20 25 30
 Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80
 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110
 Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
 435 440 445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
 450 455 460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 465 470 475 480

<210> 65
 <211> 1563
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1540)
 <223> FRXA01225

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cccgggttaa cccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
 Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
 105 110 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc	499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
120 125 130	
ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac	547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
135 140 145	
ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac	595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
150 155 160 165	
ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga	643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
170 175 180	
ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc	691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
185 190 195	
aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att	739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
200 205 210	
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc	787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
215 220 225	
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag	835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
230 235 240 245	
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag	883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
250 255 260	
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag	931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc	979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
280 285 290	
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc	1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
295 300 305	
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag	1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
310 315 320 325	
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa	1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu	
330 335 340	
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc	1171
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly	
345 350 355	
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg	1219

Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
 gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
 atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
 gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480
 cac 1563

<210> 66
 <211> 480
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 66
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 Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80
 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95
 Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125
 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140
 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160
 Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175
 Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190
 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205
 Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220
 Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240
 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415
 Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430
 Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn

435					440					445					
Glu	Phe	Gly	Tyr	Ser	Asn	Gln	Val	Ile	Arg	Ile	Val	Glu	Glu	Ile	Ala
450					455					460					
Gly	Val	Arg	Pro	Arg	Val	Tyr	Pro	Glu	Arg	Arg	Gln	Pro	Ala	Val	Leu
465					470					475					480

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<211> 1125
<212> DNA
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<223> RXA02256
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gacacattgc atttcctaca atcttttagag gagacacaac						atg acc att cgt gtt	115									
						Met Thr Ile Arg Val										
						1	5									
ggt att aac gga ttt ggc cgt atc gga cgt aac ttc ttc cgc gca gtt	163															
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Phe Phe Arg Ala Val																
						10	15	20								
ctg gag cgc agc gac gat ctc gag gta gtt gca gtc aac gac ctc acc	211															
Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala Val Asn Asp Leu Thr																
						25	30	35								
gac aac aag acc ctt tcc acc ctt ctc aag ttc gac tcc atc atg ggc	259															
Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe Asp Ser Ile Met Gly																
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cgc ctt ggc cag gaa gtt gaa tac gac gat gac tcc atc acc gtt ggt	307															
Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp Ser Ile Thr Val Gly																
						55	60	65								
ggc aag cgc atc gct gtt tac gca gag cgc gat cca aag aac ctg gac	355															
Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp Pro Lys Asn Leu Asp																
						70	75	80	85							
tgg gct gca cac aac gtt gac atc gtg atc gag tcc acc ggc ttc ttc	403															
Trp Ala Ala His Asn Val Asp Ile Val Ile Glu Ser Thr Gly Phe Phe																
						90	95	100								
acc gat gca aac gcg gct aag gct cac atc gaa gca ggt gcc aag aag	451															
Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu Ala Gly Ala Lys Lys																
						105	110	115								
gtc atc atc tcc gca cca gca agc aac gaa gac gca acc ttc gtt tac	499															
Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp Ala Thr Phe Val Tyr																
						120	125	130								

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 Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser
 135 140 145

ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta 595
 Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu
 150 155 160 165

aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca 643
 Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala
 170 175 180

tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt 691
 Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg
 185 190 195

cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca 739
 Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala
 200 205 210

gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac 787
 Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp
 215 220 225

ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg 835
 Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu
 230 235 240 245

acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca 883
 Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala
 250 255 260

atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc 931
 Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser
 265 270 275

gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc 979
 Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser
 280 285 290

atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt 1027
 Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val
 295 300 305

gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt 1075
 Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg
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 Leu Thr Glu Leu Val Ala Ser Lys Leu
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cgt 1125

<210> 68

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
 20 25 30

Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
 35 40 45

Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
 50 55 60

Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
 65 70 75 80

Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
 85 90 95

Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
 100 105 110

Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
 115 120 125

Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
 130 135 140

His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
 145 150 155 160

Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
 165 170 175

Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
 180 185 190

His Arg Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
 195 200 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 210 215 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
 225 230 235 240

Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
 245 250 255

Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
 260 265 270

Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
 275 280 285

Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
 290 295 300

Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
 305 310 315 320

Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu

325

330

<210> 69
 <211> 1338
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1315)
 <223> RXA02257

<400> 69

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gaagaatttt ttaaacaatc aaatctccaa ggagtacggc atg gct gtt aag acc 115
                                   Met Ala Val Lys Thr
                                   1 5

ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163
Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val
                                   10 15 20

cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat 211
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp
                                   25 30 35

aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa 259
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu
                                   40 45 50

ggg ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc 307
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly
                                   55 60 65

gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc 355
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser
                                   70 75 80 85

gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa 403
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu
                                   90 95 100

gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc 451
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu
                                   105 110 115

ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca 499
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala
                                   120 125 130

gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac 547
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn
                                   135 140 145

ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc 595
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr
                                   150 155 160 165

tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg 643

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Ser Val Tyr Asp	Ile Ala Lys Leu Leu Pro His Tyr Ala Gly Gly Leu	
	170 175 180	
gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag		691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu	185 190 195	
gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc		739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile	200 205 210	
ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt		787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly	215 220 225	
ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag		835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln	230 235 240 245	
cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc		883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu	250 255 260	
gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca		931
Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala	265 270 275	
tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc		979
Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser	280 285 290	
atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag		1027
Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys	295 300 305	
aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc		1075
Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly	310 315 320 325	
cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc		1123
Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly	330 335 340	
atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc		1171
Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser	345 350 355	
gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg		1219
Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu	360 365 370	
aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc		1267
Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu	375 380 385	
gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag		1315
Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln	390 395 400 405	
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 70

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Arg	Glu	Ile	Thr	Asp	Lys	Gly	Arg	Ile	Ile	Ala	Ser	Leu	Pro	Thr	Leu	35	40	45	
Lys	Ala	Leu	Ser	Glu	Gly	Gly	Ala	Lys	Val	Ile	Val	Met	Ala	His	Leu	50	55	60	
Gly	Arg	Pro	Lys	Gly	Glu	Val	Asn	Glu	Lys	Tyr	Ser	Leu	Ala	Pro	Val	65	70	75	80
Ala	Glu	Ala	Leu	Ser	Asp	Glu	Leu	Gly	Gln	Tyr	Val	Ala	Leu	Ala	Ala	85	90	95	
Asp	Val	Val	Gly	Glu	Asp	Ala	His	Glu	Arg	Ala	Asn	Gly	Leu	Thr	Glu	100	105	110	
Gly	Asp	Ile	Leu	Leu	Leu	Glu	Asn	Val	Arg	Phe	Asp	Pro	Arg	Glu	Thr	115	120	125	
Ser	Lys	Asp	Glu	Ala	Glu	Arg	Thr	Ala	Phe	Ala	Gln	Glu	Leu	Ala	Ala	130	135	140	
Leu	Ala	Ala	Asp	Asn	Gly	Ala	Phe	Val	Ser	Asp	Gly	Phe	Gly	Val	Val	145	150	155	160
His	Arg	Ala	Gln	Thr	Ser	Val	Tyr	Asp	Ile	Ala	Lys	Leu	Leu	Pro	His	165	170	175	
Tyr	Ala	Gly	Gly	Leu	Val	Glu	Thr	Glu	Ile	Ser	Val	Leu	Glu	Lys	Ile	180	185	190	
Ala	Glu	Ser	Pro	Glu	Ala	Pro	Tyr	Val	Val	Val	Leu	Gly	Gly	Ser	Lys	195	200	205	
Val	Ser	Asp	Lys	Ile	Gly	Val	Ile	Glu	Ala	Leu	Ala	Ala	Lys	Ala	Asp	210	215	220	
Lys	Ile	Ile	Val	Gly	Gly	Gly	Met	Cys	Tyr	Thr	Phe	Leu	Ala	Ala	Gln	225	230	235	240
Gly	His	Asn	Val	Gln	Gln	Ser	Leu	Leu	Gln	Glu	Glu	Met	Lys	Ala	Thr	245	250	255	
Cys	Thr	Asp	Leu	Leu	Ala	Arg	Phe	Gly	Asp	Lys	Ile	Val	Leu	Pro	Val	260	265	270	
Asp	Leu	Val	Ala	Ala	Ser	Glu	Phe	Asn	Lys	Asp	Ala	Glu	Lys	Gln	Ile	275	280	285	

Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
 290 295 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
 305 310 315 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
 325 330 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
 340 345 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
 355 360 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
 370 375 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
 385 390 395 400

Ala Ile Leu Ala Gln
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<210> 71
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1375)
 <223> RXA00235

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 ataattctag ttagctccca agttggcata ggaggccaca gtg gct gaa atc atg 115
 Val Ala Glu Ile Met
 1 5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc 163
 His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
 10 15 20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt 211
 Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
 25 30 35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac 259
 Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
 40 45 50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac 307
 Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
 55 60 65

gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat 355
 Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70 75 80 85

cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac	403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn	
90 95 100	
aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt	451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val	
105 110 115	
gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc	499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile	
120 125 130	
ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc	547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile	
135 140 145	
acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg	595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met	
150 155 160 165	
atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc	643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly	
170 175 180	
gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg	691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
185 190 195	
tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc	739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser	
200 205 210	
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc	787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly	
215 220 225	
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct	835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser	
230 235 240 245	
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc	883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser	
250 255 260	
gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca	931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro	
265 270 275	
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac	979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
280 285 290	
acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac	1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp	
295 300 305	
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag	1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys	
310 315 320 325	

aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc 1123
Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
330 335 340

acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc 1171
Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
345 350 355

tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct 1219
Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
360 365 370

gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca 1267
Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
375 380 385

gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctc cgc atc gag 1315
Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu
390 395 400 405

cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca 1363
Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
410 415 420

cgc ttt cag ggc taaataaaaag cgcttttcga cgc 1398
Arg Phe Gln Gly
425

<210> 72

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
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Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
20 25 30

Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
35 40 45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
50 55 60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
65 70 75 80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
85 90 95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
100 105 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
115 120 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
130 135 140

Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
 145 150 155 160

Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
 165 170 175

Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
 180 185 190

Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
 195 200 205

Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
 210 215 220

Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
 225 230 235 240

Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
 245 250 255

Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
 260 265 270

Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
 275 280 285

Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
 290 295 300

Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
 305 310 315 320

Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
 325 330 335

Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
 340 345 350

Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
 355 360 365

Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
 370 375 380

Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
 385 390 395 400

Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
 405 410 415

Arg Ser Ala Phe Pro Arg Phe Gln Gly
 420 425

<210> 73

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA01093

<400> 73

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 Met Gly Val Asp Arg
 1 5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163
 Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
 10 15 20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211
 Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
 25 30 35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259
 Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
 40 45 50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac 307
 Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
 55 60 65

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 Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
 70 75 80 85

gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag 403
 Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
 90 95 100

gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac 451
 Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
 105 110 115

gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc 499
 Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
 120 125 130

gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag 547
 Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
 135 140 145

ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat 595
 Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
 150 155 160 165

att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc 643
 Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
 170 175 180

gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc 691
 Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser
 185 190 195

cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt 739

Pro	Ala	Asp	Ala	Glu	Leu	Val	His	Lys	Ile	Met	Asp	Glu	Glu	Gly	Arg		
		200					205					210					
cgt	gtt	cct	gtg	atc	gcc	aag	ctg	gaa	aag	cca	gag	gct	gtc	acc	tcc	787	
Arg	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro	Glu	Ala	Val	Thr	Ser		
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ctc	gag	cca	atc	gtg	ttg	gca	ttc	gac	gcc	gtc	atg	gtt	gct	cgt	ggg	835	
Leu	Glu	Pro	Ile	Val	Leu	Ala	Phe	Asp	Ala	Val	Met	Val	Ala	Arg	Gly		
		230			235					240					245		
gac	ctc	ggc	gtt	gag	gtt	cct	ctg	gag	gag	gtt	cca	ctg	gtt	cag	aag	883	
Asp	Leu	Gly	Val	Glu	Val	Pro	Leu	Glu	Glu	Val	Pro	Leu	Val	Gln	Lys		
				250					255					260			
cgc	gca	atc	cag	att	gcc	cgt	gag	aac	gca	aag	cca	gtt	atc	gtg	gca	931	
Arg	Ala	Ile	Gln	Ile	Ala	Arg	Glu	Asn	Ala	Lys	Pro	Val	Ile	Val	Ala		
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acc	cag	atg	ctg	gat	tcc	atg	att	gag	aac	tcc	cgc	cca	acc	cgt	gcg	979	
Thr	Gln	Met	Leu	Asp	Ser	Met	Ile	Glu	Asn	Ser	Arg	Pro	Thr	Arg	Ala		
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Glu	Ala	Ser	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp	Gly	Ala	Asp	Ala	Val		
		295				300					305						
atg	ctt	tct	ggt	gaa	act	tca	gtg	ggc	aaa	gat	ccg	cac	aac	gtt	gtg	1075	
Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp	Pro	His	Asn	Val	Val		
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cgc	acc	atg	tct	cgc	att	gtt	cgc	ttc	gct	gaa	acc	gac	ggt	cgc	gtc	1123	
Arg	Thr	Met	Ser	Arg	Ile	Val	Arg	Phe	Ala	Glu	Thr	Asp	Gly	Arg	Val		
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cca	gac	ctg	acc	cac	atc	cct	cgc	act	aag	cgt	ggc	gtt	att	tcc	tac	1171	
Pro	Asp	Leu	Thr	His	Ile	Pro	Arg	Thr	Lys	Arg	Gly	Val	Ile	Ser	Tyr		
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tct	gca	cgt	gat	atc	gcc	gag	cgc	ctc	aac	gct	cgt	gca	ttg	gtt	gcg	1219	
Ser	Ala	Arg	Asp	Ile	Ala	Glu	Arg	Leu	Asn	Ala	Arg	Ala	Leu	Val	Ala		
		360				365						370					
ttc	acc	acc	tct	ggt	gat	acc	gca	aag	cgt	gtg	gct	cgt	ctg	cac	agc	1267	
Phe	Thr	Thr	Ser	Gly	Asp	Thr	Ala	Lys	Arg	Val	Ala	Arg	Leu	His	Ser		
		375				380					385						
cac	ctg	cca	ctg	ctc	gtg	ttc	act	cca	aat	gag	gca	gtt	cgc	tct	gag	1315	
His	Leu	Pro	Leu	Leu	Val	Phe	Thr	Pro	Asn	Glu	Ala	Val	Arg	Ser	Glu		
					395					400					405		
ctg	gcg	ctg	acc	tgg	ggt	gca	acc	acc	ttc	ctg	tgt	cca	cct	gtc	agc	1363	
Leu	Ala	Leu	Thr	Trp	Gly	Ala	Thr	Thr	Phe	Leu	Cys	Pro	Pro	Val	Ser		
				410					415					420			
gat	acc	gat	gac	atg	atg	cgc	gaa	gtc	gac	cgt	gct	ctt	tta	gca	atg	1411	
Asp	Thr	Asp	Asp	Met	Met	Arg	Glu	Val	Asp	Arg	Ala	Leu	Leu	Ala	Met		
				425				430					435				
cct	gag	tac	aac	aag	ggt	gac	atg	atg	gtt	gtt	gtt	gca	ggg	tcc	cct	1459	
Pro	Glu	Tyr	Asn	Lys	Gly	Asp	Met	Met	Val	Val	Val	Ala	Gly	Ser	Pro		

440 445 450
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 Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly
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 470 475

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 <213> Corynebacterium glutamicum

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 Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln
 35 40 45
 Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
 50 55 60
 Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
 65 70 75 80
 Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
 85 90 95
 Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
 100 105 110
 Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
 115 120 125
 Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
 130 135 140
 Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
 145 150 155 160
 Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
 165 170 175
 Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
 180 185 190
 Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
 195 200 205
 Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
 210 215 220
 Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
 225 230 235 240

Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val
 245 250 255

Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys
 260 265 270

Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser
 275 280 285

Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
 290 295 300

Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
 305 310 315 320

Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
 325 330 335

Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg
 340 345 350

Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
 355 360 365

Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
 370 375 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
 385 390 395 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
 405 410 415

Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
 420 425 430

Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
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<220>
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 <222> (101)..(1957)
 <223> RXN02675

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	Met	Asn	Glu	Phe	Asp	
	1				5	
cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta						163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu						
	10		15		20	
gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc						211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val						
	25		30		35	
tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat						259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His						
	40		45		50	
ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg						307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val						
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gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc						355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu						
	70		75		80	85
aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt						403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu						
	90		95		100	
tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att						451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile						
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ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act						499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr						
	120		125		130	
cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att						547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile						
	135		140		145	
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Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile						
	150		155		160	165
aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac						643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn						
	170		175		180	
gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg						691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met						
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gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca						739
Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala						
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gaa gta ggt cgc gca cga gta acc cgc gac gaa acc gga aaa gta ctg						787
Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu Thr Gly Lys Val Leu						
	215		220		225	
acg ccc gca aaa ctg tgg atc acc gcc cac ggc tcc gaa cca gtc cca						835
Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly Ser Glu Pro Val Pro						

230	235	240	245	
gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr	250	255	260	883
cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro	265	270	275	931
gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp	280	285	290	979
ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly	295	300	305	1027
acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro	310	315	320	1075
gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu	330	335	340	1123
acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr	345	350	355	1171
cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val	360	365	370	1219
ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile	375	380	385	1267
gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val	390	395	400	1315
acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile	410	415	420	1363
aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp	425	430	435	1411
ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile	440	445	450	1459
tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu	455	460	465	1507
gcc gac atc gga gat cca gta gcc gtc gaa cgc ctt ggc ctc gtc ctt Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg Leu Gly Leu Val Leu	470	475	480	1555
			485	

aaa atc gag acc atc cca ggc tac gaa ggc ctc gcc caa atc ctc ctg 1603
 Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu
 490 495 500
 acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc cgc gga gac 1651
 Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
 505 510 515
 ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc ccc caa ctg 1699
 Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val Pro Gln Leu
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 atc atg gcc ctt gcc gaa gcc gcc cac gtc cca acc atc ttg gcc acc 1747
 Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile Leu Ala Thr
 535 540 545
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 Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser Arg Ala Glu
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 Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn
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 aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc 1891
 Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
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 cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag 1939
 Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
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 <213> Corynebacterium glutamicum

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 Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
 35 40 45
 Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
 50 55 60
 Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80
 Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
 85 90 95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
 100 105 110
 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125
 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140
 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160
 Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175
 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190
 Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205
 Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
 210 215 220
 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240
 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
 245 250 255
 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
 260 265 270
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
 275 280 285
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
 290 295 300
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
 340 345 350
 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
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Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
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Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
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Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
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Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
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Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
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Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
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Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
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Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
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Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
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Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
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Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
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 <222> (1)..(363)
 <223> FRXA02675

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 Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile

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ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct			192
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser			
50	55	60	
cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc			240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val			
65	70	75	80
atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc			288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr			
85	90	95	
gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg			336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu			
100	105	110	
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Leu Arg Lys Val Lys Ser Trp Glu Glu			
115	120		
cgt			386

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 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
 50 55 60
 Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
 65 70 75 80
 Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

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<222> (101)..(1522)

<223> FRXA02695

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                                         1      5

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Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
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Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
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Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
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Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
          90                      95                      100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att 451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
          105                      110                      115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act 499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
          120                      125                      130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att 547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
          135                      140                      145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc 595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
          150                      155                      160                      165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac 643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
          170                      175                      180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg 691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
          185                      190                      195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca 739

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Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala	
200	205 210
gaa gta ggt cgc gca cga gta acc cgc gac gaa acc gga aaa gta ctg	787
Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu Thr Gly Lys Val Leu	
215	220 225
acg ccc gca aaa ctg tgg atc acc gcc cac ggc tcc gaa cca gtc cca	835
Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly Ser Glu Pro Val Pro	
230	235 240 245
gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc	883
Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr	
	250 255 260
cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca	931
Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro	
	265 270 275
gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat	979
Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp	
	280 285 290
ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc	1027
Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly	
	295 300 305
acc ctc ctg gaa cac aac tac gac cgc tcc ccg gtc tac ggc atc ccc	1075
Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro	
	310 315 320 325
gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt	1123
Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu	
	330 335 340
acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca	1171
Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr	
	345 350 355
cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc	1219
Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val	
	360 365 370
ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc	1267
Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile	
	375 380 385
gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc	1315
Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val	
	390 395 400 405
acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc	1363
Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile	
	410 415 420
aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac	1411
Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp	
	425 430 435
ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc	1459
Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile	

440	445	450	
tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc			1507
Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu			
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Ala Asp Ile Gly Asp	
470	

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 20 25 30
 Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
 35 40 45
 Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
 50 55 60
 Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80
 Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
 85 90 95
 Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
 100 105 110
 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125
 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140
 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160
 Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175
 Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190
 Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205
 Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
 210 215 220
 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240

Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
 245 250 255
 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
 260 265 270
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
 275 280 285
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
 290 295 300
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
 340 345 350
 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
 405 410 415
 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
 420 425 430
 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
 435 440 445
 Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
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 465 470

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 <223> RXA00682

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																Met Ala Asn Lys Ser
																1 5
ttc	ccc	aag	ccc	tcc	gat	ctt	cca	gtg	ccc	aag	ggc	gct	gaa	ggg	tgg	163
Phe	Pro	Lys	Pro	Ser	Asp	Leu	Pro	Val	Pro	Lys	Gly	Ala	Glu	Gly	Trp	
				10					15					20		
gaa	gat	ctg	tac	ccg	tac	tac	ctc	gtt	ttc	caa	gac	aag	ctc	atg	gat	211
Glu	Asp	Leu	Tyr	Pro	Tyr	Tyr	Leu	Val	Phe	Gln	Asp	Lys	Leu	Met	Asp	
				25					30					35		
caa	gag	aat	gag	aaa	ttc	tgg	ttc	tgc	gat	tca	cag	cac	tgg	cca	act	259
Gln	Glu	Asn	Glu	Lys	Phe	Trp	Phe	Cys	Asp	Ser	Gln	His	Trp	Pro	Thr	
				40					45					50		
gtg	ttc	aag	cct	ttt	gaa	act	atc	ggg	ggg	gaa	ttc	gct	gta	aag	tgc	307
Val	Phe	Lys	Pro	Phe	Glu	Thr	Ile	Gly	Gly	Glu	Phe	Ala	Val	Lys	Cys	
				55					60					65		
ctc	ggc	caa	tac	aac	gct	cgg	cat	ttg	atg	atc	ccg	aat	gcc	aat	ggc	355
Leu	Gly	Gln	Tyr	Asn	Ala	Arg	His	Leu	Met	Ile	Pro	Asn	Ala	Asn	Gly	
				70					75					80		
atc	gag	ttc	cgc	gtg	cat	ctg	gga	tac	ctc	tat	atg	tcc	cct	att	cca	403
Ile	Glu	Phe	Arg	Val	His	Leu	Gly	Tyr	Leu	Tyr	Met	Ser	Pro	Ile	Pro	
				90					95					100		
gtg	cct	gaa	gat	cag	att	gcg	gaa	cgc	gtc	ccc	atg	ttc	cag	gaa	cgc	451
Val	Pro	Glu	Asp	Gln	Ile	Ala	Glu	Arg	Val	Pro	Met	Phe	Gln	Glu	Arg	
				105					110					115		
atc	acg	cac	tac	ttc	caa	aac	tgg	gag	cca	atg	ctg	gca	aat	tgg	aag	499
Ile	Thr	His	Tyr	Phe	Gln	Asn	Trp	Glu	Pro	Met	Leu	Ala	Asn	Trp	Lys	
				120					125					130		
gag	cga	gta	tta	gga	acc	atc	aat	gag	ctg	gaa	tct	cta	gaa	ttc	aag	547
Glu	Arg	Val	Leu	Gly	Thr	Ile	Asn	Glu	Leu	Glu	Ser	Leu	Glu	Phe	Lys	
				135					140					145		
cca	ctg	cct	gac	tac	gtg	cct	atc	gat	gat	att	gtc	tcc	gga	aaa	gcc	595
Pro	Leu	Pro	Asp	Tyr	Val	Pro	Ile	Asp	Asp	Ile	Val	Ser	Gly	Lys	Ala	
				150					155					160		
aaa	gac	ggc	acc	gaa	gta	ctc	atg	gaa	aac	ttc	gat	cgg	ctc	att	cag	643
Lys	Asp	Gly	Thr	Glu	Val	Leu	Met	Glu	Asn	Phe	Asp	Arg	Leu	Ile	Gln	
				170					175					180		
ctc	gcc	tac	caa	aac	tgg	caa	tac	cac	ttt	gag	ttc	ctc	aac	ttg	ggg	691
Leu	Ala	Tyr	Gln	Asn	Trp	Gln	Tyr	His	Phe	Glu	Phe	Leu	Asn	Leu	Gly	
				185					190					195		
tac	atc	gct	tac	cta	gat	ttc	ttc	aat	ttc	tgc	aag	gaa	gtc	ttc	cca	739
Tyr	Ile	Ala	Tyr	Leu	Asp	Phe	Phe	Asn	Phe	Cys	Lys	Glu	Val	Phe	Pro	
				200					205					210		
gat	atc	cct	gat	caa	tca	att	tcg	atg	atg	gtt	cag	ggc	gtg	gat	atg	787
Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val	Gln	Gly	Val	Asp	Met	
				215					220					225		
gag	ctg	ttc	cgc	ccc	gat	gat	gaa	cta	aag	att	ctg	gca	cag	cta	gog	835
Glu	Leu	Phe	Arg	Pro	Asp	Asp	Glu	Leu	Lys	Ile	Leu	Ala	Gln	Leu	Ala	

230	235	240	245	
gtc gac ctt ggc ctg caa act cac ttt gcc aac ccg gat gat ccg caa				883
Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn Pro Asp Asp Pro Gln				
	250	255	260	
gct acc ttg gct gct atc gca aag gca gaa ggc ggc gcg aca tgg ata				931
Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly Gly Ala Thr Trp Ile				
	265	270	275	
gcg cgc tgg gaa gaa gca caa gat ccg tgg ttc aac ttc acc gtc ggt				979
Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe Asn Phe Thr Val Gly				
	280	285	290	
aat ggc ttc tac ggt cac gat aaa tac tgg atc gag cac ctg gaa ctt				1027
Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile Glu His Leu Glu Leu				
	295	300	305	
cca ctg ggg tac atc gcg gat tac atc cgc cgc cta gat gaa ggc caa				1075
Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg Leu Asp Glu Gly Gln				
	310	315	320	325
acc atc tcc cgc ccg aaa gat gaa ctc atc gca gaa aag gaa cgc gtg				1123
Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala Glu Lys Glu Arg Val				
	330	335	340	
gtg gaa gaa tac cgc gac ctt ttg gat gga gaa caa ctc gcg cag ttt				1171
Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu Gln Leu Ala Gln Phe				
	345	350	355	
gat gct aaa tgc ggc ctc gct gct act gca tac ccc tat gtg gaa aac				1219
Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr Pro Tyr Val Glu Asn				
	360	365	370	
cat aac ttc tac atc gag cac tgg acc atg tca gta ttt tgg cgc aaa				1267
His Asn Phe Tyr Ile Glu His Trp Thr Met Ser Val Phe Trp Arg Lys				
	375	380	385	
gta cgc gaa ctt tcc cgc act ctc cag ggc tac ggt ttc tgg gag aac				1315
Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr Gly Phe Trp Glu Asn				
	390	395	400	405
gag gat gac atg ttg tac ctc aac cgc act gaa gtc cgc gat gtc ctc				1363
Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu Val Arg Asp Val Leu				
	410	415	420	
ttc gac ctg gct act gcg tgg ggt gtc ggc gca ccc ggt ggt cca att				1411
Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala Pro Gly Gly Pro Ile				
	425	430	435	
ggc acg atc att tgg ccg gaa gaa att gag cga aga aaa gca att gtc				1459
Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val				
	440	445	450	
acc gct ttg aaa act gcc cga cca gcg cca gct ctt aac act cct cca				1507
Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro				
	455	460	465	
gag tcc atc acc gaa cct ttc acc cgc atg ctc tgg gga atc acc acc				1555
Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr				
	470	475	480	485

gaa cag gtg caa tca tgg ttg ggc aat gac gag gat gcc gaa gaa gga 1603
 Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Glu Gly
 490 495 500
 acc ctt aaa ggc atg gct gca tcc cct ggt gtg gtg gaa ggc tac gct 1651
 Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val Val Glu Gly Tyr Ala
 505 510 515
 cga gta att ctc agc gca gat gac ctt tca gaa atc cag cag gat gaa 1699
 Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu
 520 525 530
 atc ctc gtt gcc cct gta aca gca cct tct tgg ggc cca atc ttt ggc 1747
 Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp Gly Pro Ile Phe Gly
 535 540 545
 aaa atc aag gca aca gtc act gat att ggt ggc atg atg agc cat gct 1795
 Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala
 550 555 560 565
 gcg atc gtg tgc cgc gaa tac ggc ttg ccg gct gtt act gga act ggc 1843
 Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly
 570 575 580
 gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga 1891
 Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
 585 590 595
 acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa 1939
 Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
 600 605 610
 gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg 1987
 Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
 615 620 625
 gat aca cat gcc tagtccacgc actgttctta tca 2022
 Asp Thr His Ala
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<210> 82

<211> 633

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

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 20 25 30

Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
 35 40 45

Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
 50 55 60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile

65	70	75	80
Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr	85	90	95
Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro	100	105	110
Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met	115	120	125
Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu	130	135	140
Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile	145	150	155
Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe	165	170	175
Asp Arg Leu Ile Gln Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu	180	185	190
Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys	195	200	205
Lys Glu Val Phe Pro Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val	210	215	220
Gln Gly Val Asp Met Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile	225	230	235
Leu Ala Gln Leu Ala Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn	245	250	255
Pro Asp Asp Pro Gln Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly	260	265	270
Gly Ala Thr Trp Ile Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe	275	280	285
Asn Phe Thr Val Gly Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile	290	295	300
Glu His Leu Glu Leu Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg	305	310	315
Leu Asp Glu Gly Gln Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala	325	330	335
Glu Lys Glu Arg Val Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu	340	345	350
Gln Leu Ala Gln Phe Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr	355	360	365
Pro Tyr Val Glu Asn His Asn Phe Tyr Ile Glu His Trp Thr Met Ser	370	375	380
Val Phe Trp Arg Lys Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr	385	390	395
			400

Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
 405 410 415
 Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
 420 425 430
 Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
 435 440 445
 Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
 450 455 460
 Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
 465 470 475 480
 Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
 485 490 495
 Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
 500 505 510
 Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
 515 520 525
 Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
 530 535 540
 Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
 545 550 555 560
 Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
 565 570 575
 Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
 580 585 590
 Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
 595 600 605
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 Ala Ala His Gly Val Asp Thr His Ala
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 <222> (101)..(1192)
 <223> RXA00683

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aac atc ccg ttt gtc cag cgc ttc gat gaa ggc ctg gat cct gtt cta						163
Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly Leu Asp Pro Val Leu						
	10				20	
gaa gta ctc ggt ggc aag ggc gct tca cta gtc acc atg aca gat gct						211
Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val Thr Met Thr Asp Ala						
	25				35	
gga atg ccc gtt cca cct gga ttt gtg gtc act act gcc agc ttt gat						259
Gly Met Pro Val Pro Pro Gly Phe Val Val Thr Thr Ala Ser Phe Asp						
	40				50	
gaa ttc atc cgt gaa gca ggg gtt gct gaa cac atc gat aaa ttc cta						307
Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His Ile Asp Lys Phe Leu						
	55				65	
aac gat ctc gat gca gaa gat gtt aag gaa gtg gat cga gtt tct gcg						355
Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val Asp Arg Val Ser Ala						
	70				80	
atc atc cgc gat gag ctg tgc agt ctt gac gtt cca gag aat gct cgt						403
Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val Pro Glu Asn Ala Arg						
	90				95	
ttc gca gtg cac cag gct tat cgc gat ctc atg gaa cga tgc ggt ggc						451
Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met Glu Arg Cys Gly Gly						
	105				110	
gac gtc ccg gtt gct gtc cgg tca tcg gcc act gcc gaa gat ctg ccc						499
Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu Pro						
	120				125	
gat gct tcc ttc gca ggg caa cag gac acc tat ctg tgg caa gtc ggt						547
Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu Trp Gln Val Gly						
	135				140	
ttg agc gct gtc act gaa cac atc cgt aaa tgc tgg gct tcg ctg ttc						595
Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys Trp Ala Ser Leu Phe						
	150				155	
					160	
act tcc cgt gcc att atc tac cgt ctg aaa aac aac atc ccc aat gag						643
Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn Asn Ile Pro Asn Glu						
	170				175	
ggc ctc tcc atg gcg gta gtt gtt caa aaa atg gtc aac tct cgt gtc						691
Gly Leu Ser Met Ala Val Val Val Gln Lys Met Val Asn Ser Arg Val						
	185				190	
gca ggc gtg gca atc act atg aat cct tcc aac ggc gac cgc tcg aag						739
Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn Gly Asp Arg Ser Lys						
	200				205	
atc acc atc gat tcc tca tgg ggt gtt ggt gaa atg gtg gtc tca ggt						787
Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu Met Val Val Ser Gly						
	215				220	
gaa gtg aca cca gac aat atc ttg ctg gac aag atc acg ctg cag gtt						835
Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys Ile Thr Leu Gln Val						

230 235 240 245

gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc 883
 Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala
 250 255 260

acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac 931
 Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn
 265 270 275

cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct 979
 Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala
 280 285 290

aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg 1027
 Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala
 295 300 305

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 Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser
 310 315 320 325

cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act 1123
 Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr
 330 335 340

ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc 1171
 Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr
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<210> 84

<211> 364

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 84

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 20 25 30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr
 35 40 45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His
 50 55 60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val
 65 70 75 80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val
 85 90 95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met
 100 105 110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
 115 120 125
 Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
 130 135 140
 Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
 145 150 155 160
 Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
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 Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
 180 185 190
 Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
 195 200 205
 Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
 210 215 220
 Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
 225 230 235 240
 Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu
 245 250 255
 Leu Ile Pro Asp Ala Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp
 260 265 270
 Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala
 275 280 285
 Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln
 290 295 300
 Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu
 305 310 315 320
 Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys
 325 330 335
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 Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys
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<210> 85
 <211> 1860
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1837)
 <223> RXN00635

<400> 85

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gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att 163
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Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
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caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg 259
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
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Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
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Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
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Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
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Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
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Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu
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Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr
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cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg 691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala
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att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag 739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys
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aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg 787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro
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Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp	
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gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct	931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro	
265 270 275	
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Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn	
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Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly	
295 300 305	
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Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys	
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Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys	
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Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val	
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Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp	
360 365 370	
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat	1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His	
375 380 385	
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Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala	
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Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly	
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Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln	
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Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val	
455 460 465	

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Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
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Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser
490 495 500

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Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
505 510 515

ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat 1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
520 525 530

gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc 1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
535 540 545

agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg 1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met
550 555 560 565

atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca 1837
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<212> PRT
<213> Corynebacterium glutamicum

<400> 86
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35 40 45
Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
50 55 60
Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80
Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95
Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110
Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
130 135 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
145 150 155 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
165 170 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
180 185 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
195 200 205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
210 215 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
245 250 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
260 265 270

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
275 280 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
290 295 300

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
305 310 315 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
325 330 335

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
340 345 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
355 360 365

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
370 375 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
385 390 395 400

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
405 410 415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
420 425 430

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
435 440 445

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser

450	455	460
Ser Leu Gly Met Val	Lys Leu Glu Met Leu Val	Glu Gly Gln Pro Glu
465	470	475 480
Phe Gly Thr Asp His	Glu Glu Val Asn Phe Ala	Glu Ile Ala Ala Ala
	485	490 495
Ala Gly Ile Lys Ser	Val Arg Ile Thr Asp Pro	Lys Lys Val Arg Glu
	500	505 510
Gln Leu Ala Glu Ala	Leu Ala Tyr Pro Gly Pro	Val Leu Ile Asp Ile
	515	520 525
Val Thr Asp Pro Asn	Ala Leu Ser Ile Pro Pro	Thr Ile Thr Trp Glu
	530	535 540
Gln Val Met Gly Phe	Ser Lys Ala Ala Thr Arg	Thr Val Phe Gly Gly
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Pro Thr Pro		

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 <211> 552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (88)..(552)
 <223> FRXA02807

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 Met Ala His Ser Tyr Ala Glu Gln Leu
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att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 162
 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
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 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 30 35 40

gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 258
 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 45 50 55

gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 306
 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 60 65 70

ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga 354

Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg
 75 80 85
 aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag 402
 Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln
 90 95 100 105
 att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag 450
 Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
 110 115 120
 gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa 498
 Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
 125 130 135
 cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg 546
 Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
 140 145 150
 tcg gtg 552
 Ser Val
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 <210> 88
 <211> 155
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 88
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 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 20 25 30
 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 35 40 45
 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
 50 55 60
 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65 70 75 80
 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
 85 90 95
 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
 100 105 110
 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
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 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val
 145 150 155

<210> 89
 <211> 944
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(921)
 <223> FRXA00635

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cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag 96
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 20 25 30

tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct 144
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 35 40 45

cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag 192
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 50 55 60

gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac 240
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65 70 75 80

gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg 288
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 85 90 95

aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg 336
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 100 105 110

tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc 384
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 115 120 125

gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct 432
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140

cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg 480
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160

atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc 528
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175

gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt 576
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190

tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa 624
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu

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Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala			
210	215	220	
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Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu			
225	230	235	240
cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc			768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile			
245	250	255	
gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa			816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu			
260	265	270	
cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga			864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly			
275	280	285	
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Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile			
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Pro Thr Pro			
305			

<210> 90

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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20 25 30

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35 40 45

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
50 55 60

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
65 70 75 80

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
85 90 95

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
100 105 110

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
115 120 125

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 195 200 205
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 210 215 220
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 225 230 235 240
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 245 250 255
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 260 265 270
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 Pro Thr Pro
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 <223> RXN03044

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 Met Ala Arg Gly Phe
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ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163
 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
 10 15 20

cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt 211
 Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
 25 30 35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt	259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	
40 45 50	
cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt	307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	
55 60 65	
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag	355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	
70 75 80 85	
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac	403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr	
90 95 100	
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt	451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly	
105 110 115	
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Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp	
120 125 130	
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Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu	
135 140 145	
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt	595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly	
150 155 160 165	
gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc	643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser	
170 175 180	
ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag	691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln	
185 190 195	
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Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly	
200 205 210	
ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc	787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile	
215 220 225	
gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa	835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu	
230 235 240 245	
ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag	883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys	
250 255 260	
ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa	931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu	
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954

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<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

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Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
 20 25 30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
 245 250 255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
 260 265 270

Asn Ala Pro Glu Glu

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 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
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<210> 94
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 94
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 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
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 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
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Phe	Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu		
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cag	cac	atg	gat	gga	cac	tcc	cct	gtt	ttg	gct	tcc	acc	aac	gag	ggt		211
Gln	His	Met	Asp	Gly	His	Ser	Pro	Val	Leu	Ala	Ser	Thr	Asn	Glu	Gly		
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Val	Glu	Thr	Tyr	Asp	Pro	Ser	Phe	Ala	Tyr	Glu	Ile	Ala	His	Leu	Val		
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cac	cgt	ggc	atc	gac	cgc	atg	tac	ggc	cca	ggc	aag	ggt	gaa	gat	gtt		307
His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly	Lys	Gly	Glu	Asp	Val		
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atc	tac	tac	atc	acc	atc	tac	aac	gag	cca	acc	cca	cag	cca	gct	gag		355
Ile	Tyr	Tyr	Ile	Thr	Ile	Tyr	Asn	Glu	Pro	Thr	Pro	Gln	Pro	Ala	Glu		
		70			75					80					85		
cca	gaa	gga	ctg	gac	gta	gaa	ggc	ctg	cac	aag	ggc	atc	tac	ctc	tac		403
Pro	Glu	Gly	Leu	Asp	Val	Glu	Gly	Leu	His	Lys	Gly	Ile	Tyr	Leu	Tyr		
				90					95					100			
tcc	cgc	ggt	gaa	ggc	acc	ggc	cat	gag	gca	aac	atc	ttg	gct	tcc	ggt		451
Ser	Arg	Gly	Glu	Gly	Thr	Gly	His	Glu	Ala	Asn	Ile	Leu	Ala	Ser	Gly		
			105					110					115				
gtt	ggt	atg	cag	tgg	gct	ctc	aag	gct	gca	tcc	atc	ctt	gag	gct	gac		499
Val	Gly	Met	Gln	Trp	Ala	Leu	Lys	Ala	Ala	Ser	Ile	Leu	Glu	Ala	Asp		
		120					125					130					
tac	gga	gtt	cgt	gcc	aac	att	tac	tcc	gct	act	tct	tgg	gtt	aac	ttg		547
Tyr	Gly	Val	Arg	Ala	Asn	Ile	Tyr	Ser	Ala	Thr	Ser	Trp	Val	Asn	Leu		
		135				140					145						
gct	cgc	gat	ggc	gct	gct	cgt	aac	aag	gca	cag	ctg	cgc	aac	cca	ggt		595
Ala	Arg	Asp	Gly	Ala	Ala	Arg	Asn	Lys	Ala	Gln	Leu	Arg	Asn	Pro	Gly		
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gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc 643
 Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
 170 175 180
 ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag 691
 Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
 185 190 195
 atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc 739
 Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
 200 205 210
 ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc 787
 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
 215 220 225
 gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa 835
 Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
 230 235 240 245
 ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag 883
 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
 250 255 260
 ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931
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 <212> PRT
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 35 40 45
 Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60
 Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80
 Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95
 Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110
 Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
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Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
 260 265 270

Asn Ala Pro Glu Glu
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 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Ala Asp Gln Ala
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aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65
 cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85
 cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100
 cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115
 gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
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<210> 98

<211> 136

<212> PRT

<213> *Corynebacterium glutamicum*

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 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
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<212> DNA

<213> Corynebacterium glutamicum

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Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
                               10 15 20

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Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
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Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
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cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
                               55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
                               70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
                               90 95 100

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Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
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gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
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<213> Corynebacterium glutamicum

<400> 100

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 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
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<210> 101

<211> 1385

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<223> RXN03043

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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
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 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
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 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336